



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 103654

**TO: Karen A Lacourciere
Location: CM1/11D09&11E12
Art Unit: 1635
Saturday, September 13, 2003

Case Serial Number: 09/763590**

**From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov**

Search Notes

Examiner Lacourciere,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
CM-1, Rm. 6-A-06
605-1155

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html

Plate: 144 row: M column: 11

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .574

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-144M11"

/sex="Female"

/lab_host="DH10B"

/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:

ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of ECORI and ECORI Methyase. Size

selected DNA was cloned into the pBACe3.6 vector at the

ECORI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

143 a 136 c 129 g 166 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

QY

8 GUUUCGUGAGUGGUAUCAGUUCGUAACACGCGAAGUCCCGGUCGAAA 67

Db

382 GTTCCGTAGTGTAGTGTATCATCATTCGCTACACGCGAAGTCCCGGTTGAAA 323

QY

68 CCGGGC 73

Db

322 CCGGGC 317

RESULT 9

AZ989726

LOCUS

DEFINITION

2M0273K10F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0273K10 F, genomic survey sequence.

ACCESSION

AZ989726

VERSION

AZ989726.1 GI:13860953

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 695)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

TITLE

JOURNAL

COMMENT

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0273 row: K column: 10

Seq primer: CGTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 695.

Location/Qualifiers

1. .695

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0273K10"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: pMD20v; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD24 (gil4732114[gb]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

163 a 187 c 167 g 178 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

QY

8 GUUUCGUGAGUGGUAUCAGUUCGUAACACGCGAAGUCCCGGUCGAAA 67

Db

362 GTTCCGTAGTGTAGTGTATCATCATTCGCTACACGCGAAGTCCCGGTTGAAA 421

QY

68 CCGGGC 73

Db

422 CCGGGC 427

RESULT 10

CNS04T5I

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence T7 end of clone

038H13 of library A from Tetraodon nigroviridis, genomic survey

sequence.

AL306891

VERSION

AL306891.1 GI:8208133

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

1

Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Bernot,A., Fzames,C., Wincker,P., Brottier,P., Quetier,F.,

Saurin,W. and Weissenbach,J.

Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL

COMMENT

AUTHORS Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Womack,J.E., de Jong,P.J. and Lewin,H.A.
TITLE A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence
JOURNAL Unpublished
COMMENT Other_GSSs: CH240_70013.TV
 Contact: Harris Lewin
 Department of Animal Sciences
 University of Illinois at Urbana Champaign
 1201 W. Gregory Dr., Urbana, IL 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering.information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative).
 Plate: 70 row: 0 column: 13
 Seq primer: SP6
 Class: BAC ends.
FEATURES Location/Qualifiers
 source 1..201
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="bred: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_70013"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; Hereford bull LI Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
 BASE COUNT 55 a 60 c .49 g 34 t 3 others
 ORIGIN
 Query Match 45.7%; Score 64.4; DB 29; Length 201;
 Best Local Similarity 74.2%; Pred. No. 1.8e-10; Indels 0; Gaps 0;
 Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;
 QY 8 GUUUCGUGAGUGGUAUCACGUCGCUAAGCGGAAAGGUCGCCGUCGAA 67
 Db 109 GTTTCGTAGTGTAGTGGTTATCAGCTTCGCTCACACGCGAAAGTCCCGGTTCGAA 50
 QY 68 CCGGGC 73
 Db 49 CCGGGC 44
RESULT 7
 AZ115558/c 232 bp DNA linear GSS 12-MAY-2000
 LOCUS RPCI-23-16D17.TV RPCI-23 Mus musculus genomic clone RPCI-23-16D17,
 DEFINITION genomic survey sequence.
 ACCESSION AZ115558
 VERSION AZ115558.1 GI:7776690
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 232)
REFERENCE
 AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
 B., Levins,M., Megann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-23

JOURNAL Unpublished
COMMENT Other_GSSs: RPCI-23-16D17.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 16 row: D column: 17
 Seq primer: T7
 Class: BAC ends.
FEATURES Location/Qualifiers
 source 1..232
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-16D17"
 /sex="Female"
 /lab_host="DH10B"
 /clone_lib="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 55 a 57 c 54 g 66 t
 ORIGIN
 Query Match 45.7%; Score 64.4; DB 28; Length 232;
 Best Local Similarity 74.2%; Pred. No. 1.9e-10; Indels 0; Gaps 0;
 Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;
 QY 8 GUUUCGUGAGUGGUAUCACGUCGCUAAGCGGAAAGGUCGCCGUCGAA 67
 Db 180 GTTTCGTAGTGTAGTGGTTATCAGCTTCGCTCACACGCGAAAGTCCCGGTTCGAA 121
 QY 68 CCGGGC 73
 Db 120 CCGGGC 115
RESULT 8
 AZ288311/c 574 bp DNA linear GSS 27-JUL-2000
 LOCUS RPCI-23-144M11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-144M11,
 DEFINITION genomic survey sequence.
 ACCESSION AZ288311
 VERSION AZ288311.1 GI:9530097
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 574)
REFERENCE
 AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
 B., Levins,M., Megann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-23
TITLE Unpublished
JOURNAL Other_GSSs: RPCI-23-144M11.TV
COMMENT Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research

```

Db      522  GTAGTTTCGGTAGTGTATGCTATACGTTGCGCTACACGCGAAGGTCCTCCGGTTC 463
      64  GAAACCGGCGACUACAA 81
      462  GAAACCGGCGGAAACAA 445

RESULT 4
LOCUS   BH305888      720 bp      DNA      linear      GSS 30-NOV-2001
DEFINITION   CH230-179P7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
              CH230-179P7, genomic survey sequence.
ACCESSION   BH305888
VERSION     BH305888.1 GI:17218296
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 720)
AUTHORS    Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
            A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
            Jong, P. and Fraser, C.M.
            Rat BAC End Sequences from Library CHORI-230 EcoRI segment
            Unpublished
            Other GSSs: CH230-179P7.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering.information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 179 row: P column: 7
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
              1. 720
                /organism="Rattus norvegicus"
                /mol_type="genomic DNA"
                /strain="BN/SsNhsd/MCW"
                /db_xref="taxon:10116"
                /clone="CH230-179P7"
                /sex="Female"
                /cell_type="Brain"
                /clone_lib="CHORI-230 Segment 1"
                /notes="Vector: PTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                CHORI-230 Rat (BN/SsNhsd/MCW) BAC library produced by
                Pieter de Jong"

BASE COUNT      188 a      179 c      151 g      202 t
ORIGIN
Query Match      47.0%; Score 66.2; DB 28; Length 720;
Best Local Similarity 71.8%; Pred. No. 5.9e-11;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY      3  CGUUGGUUCCGUGAGUGGUUAUCGUCGUACACGCGAAGGTCCTCCGGTTC 62
      276  CATGAGTTTCGGTAGTGTATGCTATACGTTGCGCTACACGCGAAGGTCCTCCGGTTC 217
      63  CGAAACCGGGC 73
      216  CGAAACCGGGC 206

Db      522  GTAGTTTCGGTAGTGTATGCTATACGTTGCGCTACACGCGAAGGTCCTCCGGTTC 463
      64  GAAACCGGCGACUACAA 81
      462  GAAACCGGCGGAAACAA 445

RESULT 5
LOCUS   AQ030852      390 bp      DNA      linear      GSS 01-JUL-1998
DEFINITION   HS_2182_B2_H05_MF CIT Approved Human Genomic Sperm Library D Homo
              sapiens genomic clone Plate=2182 Col=10 Row=P, genomic survey
              sequence.
ACCESSION   AQ030852
VERSION     AQ030852.1 GI:3275778
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 390)
AUTHORS    Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
            Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
            Hood, L.
            Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
            Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
            99380589
            10449764
            Contact: Mahairas GS, Wallace JC, Hood L
            High throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2182 row: P column: 10
            Class: BAC ends
            High quality sequence stop: 390.
            Location/Qualifiers
              1. 390
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Plate=2182 Col=10 Row=P"
                /sex="male"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
                E-Coli DH10B"

BASE COUNT      104 a      82 c      83 g      120 t      1 others
ORIGIN
Query Match      46.4%; Score 65.4; DB 28; Length 390;
Best Local Similarity 74.6%; Pred. No. 9.7e-11;
Matches 50; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY      8  GUUUCGUGAGUGGUUAUCGUCGUACACGCGAAGGTCCTCCGGTTC 67
      163  GTTTCGGTAGTGTATGCTATACGTTGCGCTACACGCGAAGGTCCTCCGGTTC 222
      68  CCGGSCA 74
      223  CCGGSCA 229

Db      BZ920607      201 bp      DNA      linear      GSS 12-JUN-2003
DEFINITION   CH240_70013.TJ CHORI-240 Bos taurus genomic clone CH240_70013,
              genomic survey sequence.
ACCESSION   BZ920607
VERSION     BZ920607.1 GI:31645993
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 201)

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 09:43:56 ; Search time 1984.73 Seconds
(without alignments)
1726.650 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accguguuuccguagugu.....ggcacgucggaacgguuuu 141

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

```
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.6	52.9	464	10	BF244354
2	68.6	48.7	582	28	AZ062238
3	66.8	47.4	767	29	BX132357
4	66.2	47.0	720	28	BH305888

5	65.4	46.4	390	28	AQ030852
6	64.4	45.7	201	29	BZ920607
7	64.4	45.7	232	28	AZ115558
8	64.4	45.7	574	28	AZ288311
9	64.4	45.7	695	28	AZ989726
10	64.4	45.7	1101	29	CNS04751
11	64.2	45.5	595	13	BX297643
12	63.6	45.1	206	29	CNS0144U
13	63.4	45.0	590	29	C13E10
14	63.4	45.0	617	29	C111G6
15	62.6	44.8	543	13	BU712126
16	61.8	43.8	649	29	BX206800
17	61.6	43.7	488	28	AQ662870
18	61.6	43.7	761	13	BU711524
19	61.6	43.7	802	29	CNS030W4
20	61.6	43.7	897	29	CNS01XDW
21	61.6	43.7	1046	29	CNS04VSZ
22	61.6	43.7	1099	29	CNS05WVY
23	61.6	43.7	1101	29	CNS05G97
24	61.2	43.4	467	9	AA489977
25	61.2	43.4	834	13	BW174938
26	60.2	42.7	780	13	BW170857
27	60.2	42.7	789	13	BW302287
28	60	42.6	771	29	BX176182
29	60	42.6	843	29	CNS05T4P
30	59.6	42.3	1101	29	CNS05AAR
31	59	41.8	1003	29	CNS051RL
32	58.8	41.7	568	29	CNS038G0
33	58.8	41.7	692	29	CNS023IT
34	58.6	41.6	981	29	CNS04CNF
35	58.6	41.6	987	29	CNS0500S
36	58.6	41.6	1002	29	CNS056ED
37	58.4	41.4	610	29	DR16F6S
38	58.2	41.3	918	29	CNS0281P
39	58.2	41.3	946	29	CNS023IS
40	58	41.1	338	13	BW166952
41	58	41.1	363	13	BW296387
42	58	41.1	763	28	BH063051
43	57.2	40.6	935	29	CNS045M0
44	56.8	40.3	819	29	BX232148
45	55.8	39.6	936	29	CC142986

ALIGNMENTS

RESULT 1
BF244354
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BF244354 601862918F1 NIH_MGC_57 Homo sapiens CDNA clone IMAGE:4080340 5',
mRNA sequence.
BF244354.1 GI:11158272
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 464)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L10M940 row: d column: 05
High quality sequence stop: 142.

BF244354 601862918F1 NIH_MGC_57 Homo sapiens CDNA clone IMAGE:4080340 5',
mRNA sequence.
BF244354.1 GI:11158272
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 464)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L10M940 row: d column: 05
High quality sequence stop: 142.

; LENGTH: 4887 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1278..4013
US-08-005-002C-7

Query Match 21.7%; Score 30.6; DB 1; Length 4887;
Best Local Similarity 46.4%; Pred. No. 0.19;
Matches 32; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 5 UUGGUUCCGUGUGUGUUAUCACGUGCCUACACGCGAAGGUCCCGGUUCG 64
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QY 65 AAACCGGGC 73
Db 4187 ATCTGGGC 4179

Search completed: September 13, 2003, 08:06:12
Job time : 64.5109 secs

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;
;
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 629264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NO. 629264th Carolina
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGCI976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8589
;
; INFORMATION FOR SEQ ID NO: 947:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1586RP
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; US-08-998-416-947
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; Query Match 22.4%; Score 31.6; DB 3; Length 702;
; Best Local Similarity 47.1%; Pred. No. 0.04;
; Matches 33; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
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; QY 4 GUGGUUCCGUAGUGUGUGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUUC 63
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; QY 64 GAACCGGGC 73
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; Db 469 GATCCTGGGC 460
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; RESULT 14
; US-07-789-915A-7/c
; Sequence 7, Application US/07789915A
; Patent No. 5212058
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 629264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NO. 629264th Carolina
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGCI976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8589
;
; INFORMATION FOR SEQ ID NO: 947:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1586RP
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; US-08-998-416-947
;
; Query Match 22.4%; Score 31.6; DB 3; Length 702;
; Best Local Similarity 47.1%; Pred. No. 0.04;
; Matches 33; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
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; QY 4 GUGGUUCCGUAGUGUGUGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUUC 63
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; Db 529 GTGGTTTCGTCTAGTCGTTATGCGATCTGCTTAACACGACGACGTCGCCAGTTC 470
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; QY 64 GAACCGGGC 73
; ||| ||||
; Db 469 GATCCTGGGC 460
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; RESULT 14
; US-07-789-915A-7/c
; Sequence 7, Application US/07789915A
; Patent No. 5212058
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 629264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NO. 629264th Carolina
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07789,915A
; FILING DATE: 19911108
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-5091AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4887 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1278..4013
;
; US-07-789-915A-7
;
; Query Match 21.7%; Score 30.6; DB 1; Length 4887;
; Best Local Similarity 46.4%; Pred. No. 0.19;
; Matches 32; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
;
; QY 5 UUGGUUCCGUAGUGUGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUUC 64
; :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
; Db 4247 TTGGTTTCGTCTAGTCGTTATGCGATCTGCTTAACACGCGACGACGTCGCCAGTTC 4188
;
; QY 65 AAACCGGGC 73
; ||| ||||
; Db 4187 ATCCTGGGC 4179
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; RESULT 15
; US-08-005-002C-7/c
; Sequence 7, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/005,002C
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,915
; FILING DATE: 08-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: MIT-5091AAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0558
; TELEFAX: 207-363-0528
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4887 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1278..4013
;
; US-07-789-915A-7
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ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886member 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 215/154
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 171
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-512-861A-10

Query Match 30.2%; Score 42.6; DB 3; Length 171;
Best Local Similarity 67.6%; Pred. No. 2.4e-06;
Matches 75; Conservative 0; Mismatches 34; Indels 2; Gaps 1;
QY 28 AUCACGUUCGCCUUAACACACGGAAGGUCGCCGUAACCGGCGGCAUACAAACCAACA 87
DB 28 AGGUGUGGCCCAUACCCAGAGGUCGAGGUAUGGAAACCCGGA--UCGUACCGCGG 85
QY 88 CACAACACUGAUGAGGACGCGGAAGGUCGGAACGGGCGACGCGGAACCGU 138
DB 86 CACAACACUGAUGAGGACGCGGAAGGUCGGAACGGGCGGCGGCAUACCGAU 136

RESULT 7
US-08-512-861A-4
Sequence 4, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994

APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886member 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 215/154
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-512-861A-4

Query Match 29.2%; Score 41.2; DB 3; Length 146;
Best Local Similarity 70.0%; Pred. No. 7.5e-06;
Matches 70; Conservative 0; Mismatches 28; Indels 2; Gaps 1;
QY 28 AUCACGUUCGCCUUAACACACGGAAGGUCGCCGUAACCGGCGGCAUACAAACCAACA 87
DB 28 AGGUGUGGCCCAUACCCAGAGGUCGAGGUAUGGAAACCCGGA--UCGUACCGCGG 85
QY 88 CACAACACUGAUGAGGACGCGGAAGGUCGGAACGGGCGACGCGGCGGCGGCGGCGG 127
DB 86 CACAACACUGAUGAGGACGCGGAAGGUCGGAACGGGCGGCGGCGGCGGCGGCGG 125

RESULT 8
US-08-512-861A-8
Sequence 8, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886member 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 215/154
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 146

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Query Match          49.5%; Score 69.8; DB 3; Length 132;
Best Local Similarity 72.6%; Pred. No. 2.9e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGUGAGUGUUAUCACGUCGUAACACGCGGAAAGGUCGCCGG 60
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Db 11 ACCGTTGTTCCGAGTAGTGTATCAGTTCGCTCACACGCGGACGTCGCCGG 70
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QY 61 UUCGAAACCGGGC 73
    :|||||
Db 71 TTCGAAACCGGGC 83

RESULT 4
PCT-US94-05700-17
; Sequence 17, Application PC/TUS9405700
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: RIBOZYME GENE THERAPY FOR HIV INFECTION AND AIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 NORTH FIGUEROA STREET
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05700
; FILING DATE: 17 MAY 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 97
; OTHER INFORMATION: /note= "W" = INTERNAL NUCLEOTIDE
; OTHER INFORMATION: SEQUENCE="
PCT-US94-05700-17

Query Match          49.5%; Score 69.8; DB 5; Length 133;
Best Local Similarity 72.6%; Pred. No. 2.9e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

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QY 61 UUCGAAACCGGGC 73
    :|||||
Db 71 TTCGAAACCGGGC 83

RESULT 5
US-08-512-861A-6
; Sequence 6, Application US/08512861A
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; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-6

Query Match          30.2%; Score 42.6; DB 3; Length 171;
Best Local Similarity 67.6%; Pred. No. 2.4e-06;
Matches 75; Conservative 0; Mismatches 34; Indels 2; Gaps 1;

QY 28 AUCAGUUCGCCUAACACGCGGAAAGUCCCGGUAACCGGCGCACUACAACCAACA 87
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QY 88 CACAACACUGAUGAGGACGCGGAAAGGUGCGGACGCGGCGGAAACCGU 138
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Db 86 CACAACACUGAUGAGGACGCGGAAAGGUGCGGACGCGGAGGAGUACGUAACG 136
    |||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
US-08-512-861A-10
; Sequence 10, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
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OTHER INFORMATION: /note= "insertion location of
foreign gene in pol III
OTHER INFORMATION: transcription cassette in
vector pMT"
US-08-245-742A-17

Query Match 49.5%; Score 69.8; DB 1; Length 132;
Best Local Similarity 72.6%; Pred. No. 2.9e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUUGUUCCGUGAGUGUUAUCAGUUGCCUACACGCCGAAAGGUCGCCGG 60
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Db 11 ACCGTGGTTTCGTAGTGTATGCTGCTATCAGTTCGCTCAGACGCCGAAAGGTCGCCGG 70

QY 61 UUCGAAACCGGC 73
Db 71 TTCGAAACCGGC 83

RESULT 2
US-08-465-483-17
Sequence 17, Application US/08465483
Patent No. 5811275
GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yamada, Osamu
APPLICANT: Ojwang, Joshua O.
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,483
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,465
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,742
FILING DATE: 17-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 2307E-567-11
TELEPHONE: (415) 543-9600
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: (96^97)
OTHER INFORMATION: /note= "insertion location of
foreign gene in pol III
OTHER INFORMATION: transcription cassette in
vector pMT"

OTHER INFORMATION: foreign gene in pol III
OTHER INFORMATION: transcription cassette in
vector pMT"
US-08-465-483-17

Query Match 49.5%; Score 69.8; DB 1; Length 132;
Best Local Similarity 72.6%; Pred. No. 2.9e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUUGUUCCGUGAGUGUUAUCAGUUGCCUACACGCCGAAAGGUCGCCGG 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 ACCGTGGTTTCGTAGTGTATGCTGCTATCAGTTCGCTCAGACGCCGAAAGGTCGCCGG 70

QY 61 UUCGAAACCGGC 73
Db 71 TTCGAAACCGGC 83

RESULT 3
US-08-876-996-17
Sequence 17, Application US/08876996
Patent No. 6132962
GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yamada, Osamu
APPLICANT: Ojwang, Joshua O.
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,996
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,742
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 2307E-567-10
TELEPHONE: (415) 543-9600
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: (96^97)
OTHER INFORMATION: /note= "insertion location of
foreign gene in pol III
OTHER INFORMATION: transcription cassette in
vector pMT"

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 07:56:11 ; Search time 47.5109 Seconds
(without alignments)
1309.911 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accguguuuccguagugu.....ggcagcuggaaacgguuuu 141

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2.6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2.6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2.6/ptodata/2/ina/5A_COMB.seq.*

4: /cgn2.6/ptodata/2/ina/5B_COMB.seq.*

5: /cgn2.6/ptodata/2/ina/PTUS_COMB.seq.*

6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69.8	49.5	132	1	US-08-245-742A-17
2	69.8	49.5	132	1	US-08-465-483-17
3	69.8	49.5	132	3	US-08-876-996-17
4	69.8	49.5	133	5	PCT-US94-05700-17
5	42.6	30.2	171	3	US-08-512-861A-6
6	42.6	30.2	171	3	US-08-512-861A-10
7	41.2	29.2	146	3	US-08-512-861A-4
8	41.2	29.2	146	3	US-08-512-861A-8
9	41.2	29.2	167	3	US-08-512-861A-14
10	34.4	24.4	1483	1	US-08-270-076A-2
11	34.2	24.3	186	4	US-09-107-532A-488
12	32.6	23.1	1230025	4	US-09-198-452A-1
13	31.6	22.4	702	3	US-08-998-416-947
14	30.6	21.7	4887	1	US-07-789-915A-7
15	30.6	21.7	4887	1	US-08-005-002C-7
16	30.6	21.7	4887	1	US-08-487-203A-7
17	30	21.3	4792	4	US-09-189-462-5
18	29.8	21.1	1664976	4	US-08-916-421B-1
19	29.6	21.0	648	3	US-08-998-416-111
20	29.4	20.9	729	3	US-08-998-416-607
21	29	20.6	1664976	4	US-08-916-421B-1
22	28.8	20.4	5109	4	US-08-930-055A-2
23	28.6	20.3	1683	3	US-08-983-045-3
24	28.6	20.3	124884	4	US-09-661-596A-76
25	28.6	20.3	1230025	4	US-09-198-452A-1
26	28.4	20.1	2798	4	US-09-336-115C-1
27	28.4	20.1	38155	4	US-09-453-702B-79

c 28 28.4 20.1 43804 4 US-09-171-461-1
29 19.9 2185 1 US-08-173-508-3
30 28 2185 2 US-08-265-310-3
31 28 2185 3 US-08-951-742-3
32 27.6 19.6 1756 2 US-08-465-640-1
33 27.6 19.6 16885 1 US-08-390-878-16
34 27.6 19.6 4403765 3 US-09-103-840A-2
35 27.6 19.6 4411529 3 US-09-103-840A-1
36 27.4 19.4 21338 4 US-08-961-527-20
37 27.2 19.3 9472 4 US-08-150-204E-96
38 27 19.1 13865 3 US-09-009-217-11
39 27 19.1 13865 3 US-09-009-656-11
40 26.8 19.0 36241 4 US-08-311-731A-134
41 26.6 18.9 724 1 US-08-599-252-98
42 26.6 18.9 724 5 PCT-US96-06352-98
43 26.6 18.9 724 5 PCT-US96-06583-98
44 26.6 18.9 1178 3 US-08-861-774E-93
45 26.6 18.9 4403765 3 US-09-103-840A-2

ALIGNMENTS

RESULT 1

US-08-245-742A-17
; Sequence 17, Application US/08245742A
; Patent No. 5670361

GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie

APPLICANT: Yu, Mang

APPLICANT: Yamada, Osamu

APPLICANT: Ojwang, Joshua O.

APPLICANT: Leavitt, Mark

APPLICANT: Ho, Anthony

TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection

TITLE OF INVENTION: and AIDS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Tower

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/245,742A

FILING DATE: 17-MAY-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/062,465

FILING DATE: 17-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 2307E-567-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: (96^97)

Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 20, Appli
Sequence 96, Appli
Sequence 11, Appli
Sequence 134, Appli
Sequence 98, Appli
Sequence 98, Appli
Sequence 93, Appli
Sequence 2, Appli

QY 1 ACCGUUGUUCGAGUAGUGGUUACGUGCGUACGCGGAAAGGUCGCCGG 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 539 ATCATCAGTTCCGAGTAGTGTAGTGTATACGTTCCGCTAACACGCGAAAGGTCGCCGG 480
 QY 61 UUCGAAACCGGCG 73
 :||| |||||
 Db 479 TTCGAGCCCGGCG 467

RESULT 15

BU712126 543 bp mRNA linear EST 12-FEB-2003
 LOCUS SJAAAWA07 Adult sjc 7/94 Schistosoma japonicum cDNA, mRNA sequence.
 DEFINITION BU712126
 ACCESSION
 VERSION BU712126.1 GI:28319513
 KEYWORDS EST
 SOURCE Schistosoma japonicum
 ORGANISM Schistosoma japonicum
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 REFERENCE 1 (bases 1 to 543)
 AUTHORS Hu, W., Yan, Q., Shen, D., Liu, F., Xu, X., Zhu, Z., Zhang, X., Wang, J.,
 Sun, J., Xu, X., Wang, Z., Zeng, L., Rong, Y., Wu, X., Qu, J., Xu, Z.,
 Huang, J., Ma, Y., Wang, S., Wang, Z., Xue, C., Feng, Z., Chen, Z., and Han
 Z.

Expressed sequence tags from adults of Schistosoma japonicum

Unpublished
 Contact: Zequang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn.
 Location/Qualifiers

FEATURES

SOURCE

1. .543
 /organism="Schistosoma japonicum"
 /mol_type="mRNA"
 /strain="Chinese (Anhui) strain"
 /db_xref="taxon:6182"
 /sex="Male and female"
 /tissue_type="Whole body"
 /dev_stage="Adult worms"
 /lab_host="Mouse and rabbit"
 /clone_lib="Adult sjc 7/94"
 /note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
 XhoI I; Several hundred adult Schistosoma japonicum (Anhui
 , P. R. China, strain), of mixed sex, were perfused from
 the mesenteries of experimentally infected mice and
 rabbits at the Queensland Institute of Medical Research,
 Brisbane, Australia (QIMR), and stored for several months
 in liquid nitrogen. Subsequently, mRNA was isolated at the
 QIMR from lysates of these worms by oligo dT
 chromatography, using a kit from Pharmacia. The mRNA was
 then shipped to Clontech, Palo Alto, CA, USA, who
 constructed a cDNA library. First strand synthesis was
 primed with an oligo-dT-primer and synthesized using
 M-MLV reverse transcriptase. Second strand synthesis was
 accomplished with RNase H and T4 DNA polymerase. The
 double stranded cDNA was ligated to EcoRI linkers,
 digested with EcoRI and XhoI, and ligated into the
 phagemid vector lambda ZAP II XR. After construction of
 this directional library by Clontech, it was returned to
 the QIMR. During analysis of the library at the QIMR, we
 have found that a small percentage, 2% to 3%, of the
 clones contain inserts that appear to be highly homologous
 to sequences from salmonoid fishes, as determined by
 homology comparisons using BLAST and by Southern
 hybridization analysis to genomic DNA from salmon (Sigma
 Chemical Co., St. Louis, MO) under stringent washing
 conditions. The remainder of the clones appear to contain
 S. japonicum sequences."

BASE COUNT 183 a 109 c 90 g 160 t 1 others

ORIGIN
 Query Match 46.4%; Score 62.6; DB 13; Length 543;
 Best Local Similarity 69.6%; Pred. No. 3.6e-10;
 Matches 48; Conservative 17; Mismatches 4; Indels 0; Gaps 0;
 QY 5 UUGGUUCCGAGUGUAGUGGUUACGUGCGUACGCGGAAAGGUCGCCGGUUGG 64
 : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 453 TAGGTTCCGTAAGTAGTGTATACATTCGCTCACACGCGAAGGTCGCCGGTTGG 512
 QY 65 AAACCCGGCG 73
 ||||| |||
 Db 513 AAACCCGGCG 521
 Search completed: September 13, 2003, 11:44:41
 Job time : 1907.27 secs

genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.

FEATURES

SOURCE

1. .206
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="219P01"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG219CH01SP1-end :
PUC-ori"

BASE COUNT 58 a 42 c 48 g 46 t 12 others
ORIGIN

Query Match 47.1%; Score 63.6; DB 29; Length 206;
Best Local Similarity 74.2%; Pred. No. 1.3e-10;
Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY 8 GUUCCGUGAGUGGUAUCACGUCGUAACACGCGAAAGGUCGCCGUGCGAA 67

Db 172 GTTCGGTAGTGTAGTGTATACGTTCCCTISACACGCGAAAGTCCCGGTTGCGAA 113

QY 68 CGCGGC 73

Db 112 CGCGGC 107

RESULT 13

C13E10/c

LOCUS

DEFINITION C13E10 590 bp DNA linear GSS 03-DEC-2000
Ciona intestinalis genomic fragment, clone 3E10, genomic survey

ACCESSION

VERSION AJ227180.1 GI:2951004

KEYWORDS

GSS: genome survey sequence.

SOURCE

Ciona intestinalis

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

Simmen,M.W., Leitgeb,S., Clark,V.H., Jones,S.J., Harris,B.R.,

Clark,V.H. and Bird,A.

Gene number in an invertebrate chordate, Ciona intestinalis

Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)

98208558

PUBMED 9539755

REFERENCE 2

Simmen,M.W., Leitgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,

Clark,V.H. and Bird,A.

Nonmethylated transposable elements and methylated genes in a

chordate genome

Science 283 (5405), 1164-1167 (1999)

99148102

PUBMED 10024242

REFERENCE 3

Simmen,M.W. and Bird,A.

Sequence analysis of transposable elements in the sea squirt, Ciona

intestinalis

Mol. Biol. Evol. 17 (11), 1685-1694 (2000)

20523971

PUBMED 11070056

REFERENCE 4 (bases 1 to 590)

Clark,V.H., Leitgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and

Bird,A.P.

Direct Submission

Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's

Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:

VCLARK@serv0.bio.ed.ac.uk

Vector: pBluescript KS.

COMMENT

FEATURES

SOURCE

1. .590

/organism="Ciona intestinalis"

/mol_type="genomic DNA"

/db_xref="taxon:7719"

BASE COUNT 197 a 109 c 120 g 164 t
ORIGIN

Query Match 47.0%; Score 63.4; DB 29; Length 590;
Best Local Similarity 68.5%; Pred. No. 2e-10;
Matches 50; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGUGAGUGUAUCACGUCGUAACACGCGAAAGGUCGCCG 60

Db 441 ATCATCAGTTCCGTAGTGTATACGTTCCCTAACACGCGAAAGGTCGCCG 382

QY 61 UUCGAAACCGGCG 73

Db 381 TTCGAGCCCGGC 369

RESULT 14

C11I6/c

LOCUS

DEFINITION C11I6 617 bp DNA linear GSS 03-DEC-2000
Ciona intestinalis genomic fragment, clone 1I66, genomic survey

ACCESSION

VERSION AJ226216.1 GI:2949677

KEYWORDS

GSS: genome survey sequence.

SOURCE

Ciona intestinalis

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

Simmen,M.W., Leitgeb,S., Clark,V.H., Jones,S.J., Harris,B.R.,

Clark,V.H. and Bird,A.

Gene number in an invertebrate chordate, Ciona intestinalis

Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)

98208558

PUBMED 9539755

REFERENCE 2

Simmen,M.W., Leitgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,

Clark,V.H. and Bird,A.

Nonmethylated transposable elements and methylated genes in a

chordate genome

Science 283 (5405), 1164-1167 (1999)

99148102

PUBMED 10024242

REFERENCE 3

Simmen,M.W. and Bird,A.

Sequence analysis of transposable elements in the sea squirt, Ciona

intestinalis

Mol. Biol. Evol. 17 (11), 1685-1694 (2000)

20523971

PUBMED 11070056

REFERENCE 4 (bases 1 to 617)

Clark,V.H., Leitgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and

Bird,A.P.

Direct Submission

Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's

Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:

VCLARK@serv0.bio.ed.ac.uk

Vector: pBluescript KS.

COMMENT

FEATURES

SOURCE

1. .617

/organism="Ciona intestinalis"

/mol_type="genomic DNA"

/db_xref="taxon:7719"

/clone="1I66"

/dev_stage="adult"

/dev_stage="adult"

BASE COUNT 200 a 113 c 126 g 176 t 2 others

ORIGIN

Query Match 47.0%; Score 63.4; DB 29; Length 617;

Best Local Similarity 68.5%; Pred. No. 2e-10;

Matches 50; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

REFERENCE	1 (bases 1 to 201)	Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Womack,J.E., de Jong,P.J. and Lewin,H.A.
AUTHORS		
TITLE	A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence	
JOURNAL	Unpublished	
COMMENT	Other_GSSs: CH240_70013.TV Contact: Harris Lewin Department of Animal Sciences University of Illinois at Urbana Champaign 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5398 Fax: 217 244 5617 Email: h-lewin@uiuc.edu Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@email.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderinginformation.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by University of Illinois at Urbana Champaign, USA with funds provided by grant NO. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative) Plate: 70 row: O column: 13 Seq primer: SP6 Class: BAC ends.	
FEATURES	location/Qualifiers	
source	1..201	/organism="Bos taurus" /mol_type="genomic DNA" /strain="breed: Hereford" /db_xref="taxon:9913" /clone="CH240_70013" /sex="Male" /cell_type="Blood" /clone_lib="CHORI-240" /notes="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
BASE COUNT	55 a 60 c 49 g 34 t 3 others	
ORIGIN		
Query Match	47.7%; Score 64.4; DB 29; Length 201;	
Best Local Similarity	74.2%; Pred. No. 7.2e-11;	
Matches	49; Conservative 16; Mismatches 1;	Indels 0; Gaps 0;
QY	8 GUUUCUGAGUGAGUGGUUAUCAGUUCGCUACACGCGAAGAGGUCGCCGUUCGAAA 67	
DDb	109 GTTTCGTAGTGTAGTGGTATACAGCTTCGCTCACGCGAAGAGGTCGCCGGTTCGAAA 50	
QY	68 CCGGGC 73	
DDb	49 CCGGGC 44	
RESULT 8		
AZ115558/c		
LOCUS	AZ115558 232 bp DNA linear GSS 12-MAY-2000	
DEFINITION	RPCI-23-16D17.TV RPCI-23 Mus musculus genomic clone RPCI-23-16D17.	
ACCESSION	AZ115558	
VERSION	AZ115558.1	GI:7776690
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 232) Zhao,S., Niernan,W., Feildblyum,T., Malek,J., Shatsman,S., Akinret B., Lewins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.	

FEATURES

Source

Location/Qualifiers

1. .464
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4080340"
 /tissue_type="glioblastoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NH_MGC_57"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site:1: SfiI (ggccctcgccgc); Site:2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, G or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
 BASE COUNT 138 a 110 c 160 g 55 t 1 others
 ORIGIN

Query Match 52.6%; Score 71; DB 10; Length 464;
 Best Local Similarity 62.5%; Pred. No. 5.6e-13;
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 2 CCGUGGUUCCGAGUGAGUGGUUAUCACGUCGUAACACGCGAAAGGUCGCCGGU 61
 ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 27 CCGGGGTTTCGTAGTGTAGTGTATCATCGTTCGCTAACACGCGAAAGGTTCCCGGT 86
 ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 62 UCGAAACCGGCGACACACACACACUGAGGAGCGGAAGGUCGCGAA 113
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 87 TCGAAACCGGCGGACACACACACACACACACACACACACACACACACACAA 138

RESULT 2
 LOCUS AZ062238 582 bp DNA linear GSS 30-MAR-2000
 DEFINITION RPCI-23-404J7-TV RPCI-23 Mus musculus genomic clone RPCI-23-404J7,
 genomic survey sequence.
 ACCESSION AZ062238
 VERSION AZ062238.1 GI:7353487
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
 , B., Levins, M., McGann, S., Tsengaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished
 COMMENT Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@tigr.org), please contact Pieter de Jong (pieter@tigr.org). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 404 row: J column: 7
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers 1. .582

FEATURES

Source

Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-404J7"
 /sex="Female"
 /lab_host="DH10B"
 /clone_lib="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1: ECORI; Site:2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of ECORI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL life technologies)."
 BASE COUNT 154 a 125 c 163 g 140 t
 ORIGIN

Query Match 49.8%; Score 67.2; DB 28; Length 582;
 Best Local Similarity 68.8%; Pred. No. 1.1e-11;
 Matches 55; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 2 CCGUGGUUCCGAGUGAGUGGUUAUCACGUCGUAACACGCGAAAGGUCGCCGGU 61
 ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 53 CCAGTGGTTTCGTAGTGTAGTGTATCATCGTTCGCTAACACGCGAAAGGTTCCCGGT 112
 ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 62 UCGAAACCGGCGGACACACAA 81
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 113 TCGAAACCGGCGGACACAA 132

RESULT 3

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

BX132357 767 bp DNA linear GSS 28-JAN-2003
 Danio rerio genomic clone DKEY-90F23, genomic survey sequence.
 BX132357
 BX132357.1 GI:27963631
 GSS:
 Danio rerio (zebrafish)
 Danio rerio
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 767)
 Humphray, S.J., Huckle, E. and Durham, J.L.
 Direct Submission
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Unpublished
 This sequence was generated from the SP6 end of BAC 90F23. 90F23 is
 part of the Daniokey BAC Library created by R. Plasterk and N.V.
 Keygene. Further details:
 http://www.sanger.ac.uk/projects/D_rerio/.

FEATURES

Source

Location/Qualifiers

I. .767

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="DKEY-90F23"

/tissue_type="testis"

/note="vector pindigobac-536"

BASE COUNT 244 a 144 c 121 g 258 t
 ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

Db

QY

GSS

GSS

GSS

GSS

GSS

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 09:43:56 ; Search time 1900.27 Seconds
(without alignments)
1726.650 Million cell updates/sec

Title: US-09-763-590-1

Perfect score: 135

Sequence: 1 accgugguuuccuagugu.....ggcacgucggaacgguuuu 135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estl:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_estfun:*

15: em_eston:*

16: em_gss_hum:*

17: em_gss_inv:*

18: em_gss_pln:*

19: em_gss_vrt:*

20: em_gss_fun:*

21: em_gss_mam:*

22: em_gss_mus:*

23: em_gss_pro:*

24: em_gss_rod:*

25: em_gss_phg:*

26: em_gss_vrl:*

27: gb_gss1:*

28: gb_gss2:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	71	52.6	464	10	BF244354
2	67.2	49.8	582	28	AZ062238
c 3	66.8	49.5	767	29	BX132357
c 4	66.2	49.0	720	28	BH305888

5	65.4	48.4	390	28	AQ030852
6	64.8	48.0	695	28	AZ989726
c 7	64.4	47.7	201	29	BZ920607
c 8	64.4	47.7	232	28	AZ115558
c 9	64.4	47.7	574	28	AZ288311
c 10	64.4	47.7	1101	29	CNS04751
c 11	64.2	47.6	595	13	BX297643
c 12	63.6	47.1	206	29	CNS01240
c 13	63.4	47.0	590	29	C13E10
c 14	63.4	47.0	617	29	C11IG6
15	62.6	46.4	543	13	BU712126
16	61.8	45.8	649	29	BX206800
17	61.6	45.6	418	28	AO662870
c 18	61.6	45.6	761	13	BU711524
19	61.6	45.6	802	29	CNS030M4
20	61.6	45.6	897	29	CNS01XDM
21	61.6	45.6	1046	29	CNS04Y52
22	61.6	45.6	1099	29	CNS05MVY
23	61.6	45.6	1101	29	CNS05G97
c 24	61.2	45.3	467	9	AA489977
c 25	61.2	45.3	834	13	BM174938
c 26	60.2	44.6	771	29	BX176182
c 27	60.2	44.6	780	13	BM170857
c 28	60.2	44.6	789	13	BW302287
29	60.4	44.4	843	29	CNS0574P
30	59.6	44.1	1101	29	CNS05AAR
31	59	43.7	1003	29	CNS051R1
c 32	58.8	43.6	568	29	CNS038G0
c 33	58.8	43.6	692	29	CNS023IT
c 34	58.6	43.4	981	29	CNS04CNF
c 35	58.6	43.4	987	29	CNS0500S
36	58.6	43.4	1002	29	CNS056ED
c 37	58.4	43.3	610	29	DR16F6S
c 38	58.2	43.1	918	29	CNS0281P
c 39	58.2	43.1	946	29	CNS0231S
c 40	58	43.0	338	13	BM166952
c 41	58	43.0	383	13	BW296387
c 42	57.2	42.4	763	28	BH063051
c 43	57.2	42.4	935	29	CNS045M0
c 44	56.2	41.6	791	29	CC127410
c 45	55.8	41.3	819	29	BX232148

ALIGNMENTS

RESULT 1
BF244354
LOCUS
DEFINITION 601862918F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080340 5',
464 bp mRNA linear EST 14-NOV-2000
BF244354
mRNA sequence.
ACCESSION
VERSION BF244354.1 GI:11158272
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 464)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: graphs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM940 row: d column: 05
High quality sequence stop: 142.

Qy 68 CCGGGCACUACAAACA 83
|||||
Db 170 CCGGTCGGGACCGCCA 185

Search completed: September 13, 2003, 09:43:36
Job time : 166.25 secs

US-10-027-632-150960

[illegible]

RESULT.7 9

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US-10-027-632-135532/c
; Sequence 135532, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 135532
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-135532

```

	Query Match	37.5%	Score 50.6;	DB 13;	Length 603;
	Best Local Similarity	61.5%;	Pred. No. 3e-08;		
	Matches 40;	Conservative 16;	Mismatches 9;	Indels 0;	Gaps 0;
QY	8	GUUUCGGAGUGUAGUGGUUAUCACGUCGUCUACACGCGAAAGGUCGCCGCGUUCGAAA	67		
Db	136	GTTTCTGTAGTAGTGTGGTTATCAGTTAGTTCACAGGTGAAAGGTCCTGTTGCGAAA	77		
QY	68	CCGGG	72		
Db	76	CCAGG	72		

RESULT 10

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US-10-027-632-135520
; Sequence 135520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676

```

```

, PRIOR FILING DATE: 2000-04-20
, PRIOR APPLICATION NUMBER: US 60/193,483
, PRIOR FILING DATE: 2000-03-29
, PRIOR APPLICATION NUMBER: US 60/185,218
, PRIOR FILING DATE: 2000-02-24
, PRIOR APPLICATION NUMBER: US 60/167,363
, PRIOR FILING DATE: 1999-11-23
, PRIOR APPLICATION NUMBER: US 60/156,358
, PRIOR FILING DATE: 1999-09-28
, PRIOR APPLICATION NUMBER: US 60/146,002
, PRIOR FILING DATE: 1999-08-09
, NUMBER OF SEQ ID NOS: 325720
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 135520
, LENGTH: 817
, TYPE: DNA
, ORGANISM: Human
US-10-027-632-135520

```

Query Match	37.0%;	Score 50;	DB 13;	Length 817;
Best Local Similarity	58.8%;	17;	Mismatches 11;	
Matches 40;	Conservative	11;	Indels	0; Gaps 0;
QY	6	UGGUUUCGUAUGUGAGUGUUUAUCAGUUCGCUAACACGCGAAAGGUCCCGGUUGCA	65	
Db	304	TGGCTTCCTGTAATAGTGGTTATCAGATTTCGCTCACATGAAGGTCACCAATTGA	363	
QY	66	AAACCGGCG	73	
Db	364	GACCGGCG	371	

RESULT 11

```

US-10-027-632-148440/c
; Sequence 148440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148440
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-148440

```

	Query Match	35.94;	Score 48.4;	DB 13;	Length 871;
	Best Local Similarity	59.5%;	Pred.No. 2e-07;		
	Matches	44;	Conservative	14;	Mismatches 16; Indels 0; Gaps 0;
QY	8	GUUCCGUGAGUGAUGUAUCACGUCGCCAACACCGAAAGGUCGCCGGUUCGA	67		
		: :			
Db	823	GTTCCGTAGTGTAGTGCTATCATGTTCGCCTCACACGCGAAAGTCCCGTTTCA	764		
QY	68	CCGGCACAUCACAA	81		

RESULT 7
US-10-027-632-150959

US-09-974-974-17
 ; Sequence 17, Application US/09974974
 ; Publication No. US20030013095A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kazunari TAIRA
 ; APPLICANT: Masashi WARASHINA
 ; APPLICANT: Tomoko WARASHINA
 ; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
 ; target RNA by recognizing another molecule
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/974,974
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: JP 2000-313320
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 138
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal T-MEL
 ; US-09-974-974-17

Query Match 61.3%; Score 82.8; DB 11; Length 138;
 Best Local Similarity 97.7%; Pred. No. 5.9e-20;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUUCUCCGAGUGAGUGUUAUCACGUCUCCUAACACGCGAAAGGUCGCCGG 60
 |||||
 Db 1 ACCGUGUUCUCCGAGUGAGUGUUAUCACGUCUCCUAACACGCGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGCGACUACACAA 86
 |||||
 Db 61 UUCGAAACCGGCGACUACAAACCA 86

RESULT 3
 US-10-027-632-13958/c
 ; Sequence 13958, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13958
 ; LENGTH: 704
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-027-632-13958

Query Match 48.7%; Score 65.8; DB 13; Length 704;
 Best Local Similarity 71.8%; Pred. No. 1.1e-13;
 Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGUUGUUCUCCGAGUGAGUGUUAUCACGUCUCCUAACACGCGAAAGGUCGCCGGU 62
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 62
 Db 301 YCAGGTTTCCTAGTGTAGTGTATCAGGTCGCTCACACGCGAAAGGTCCTCCGGTT 242

QY 63 CGAAACCGGGC 73
 |||||
 Db 241 CGAAACCGGGC 231

RESULT 4
 US-10-027-632-13959/c
 ; Sequence 13959, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13959
 ; LENGTH: 704
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-027-632-13959

Query Match 48.7%; Score 65.8; DB 13; Length 704;
 Best Local Similarity 71.8%; Pred. No. 1.1e-13;
 Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGUUGUUCUCCGAGUGAGUGUUAUCACGUCUCCUAACACGCGAAAGGUCGCCGGU 62
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 62
 Db 301 YCAGGTTTCCTAGTGTAGTGTATCAGGTCGCTCACACGCGAAAGGTCCTCCGGTT 242

QY 63 CGAAACCGGGC 73
 |||||
 Db 241 CGAAACCGGGC 231

RESULT 5
 US-10-027-632-13960/c
 ; Sequence 13960, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 08:02:46 ; Search time 146.25 Seconds
(without alignments)
2241.006 Million cell updates/sec

Title: US-09-763-590-1

Perfect score: 135

Sequence: 1 accgugguuucguagu.....ggcagcugcgaaacgguuu 135

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.8	61.3	88	11	US-09-974-974-5
2	82.8	61.3	138	11	US-09-974-974-17
3	85.8	48.7	704	13	US-10-027-632-13958
4	65.8	48.7	704	13	US-10-027-632-13959
5	65.8	48.7	704	13	US-10-027-632-13960
6	65.8	48.7	704	13	US-10-027-632-13961
7	61.2	45.3	818	13	US-10-027-632-150959
8	61.2	45.3	818	13	US-10-027-632-150960
9	50.6	37.5	603	13	US-10-027-632-135532
10	50.6	37.5	603	13	US-10-027-632-135520
11	48.4	35.9	871	13	US-10-027-632-139520
12	41.6	30.8	118067	15	US-10-081-327-32
13	40.2	29.8	322	13	US-10-027-632-272410
14	38.6	28.6	2126	12	US-10-325-107-59
15	37.6	27.9	9399	9	US-09-842-552-100
16	37.6	27.9	2336	9	US-09-842-552-102

17	37.4	27.7	5048	11	US-09-884-465A-2	Sequence 2, Appli
c 18	36.2	26.8	740	10	US-09-070-927A-846	Sequence 846, App
c 19	36	26.7	440	9	US-09-864-761-10165	Sequence 10165, A
c 20	35.8	26.5	400	8	US-08-781-986A-3707	Sequence 3707, Ap
c 21	35.6	26.4	9425	8	US-08-781-986A-87	Sequence 87, Appl
c 22	35	25.9	400	8	US-08-781-986A-3777	Sequence 3777, Ap
c 23	34.8	25.8	400	8	US-08-781-986A-3809	Sequence 3809, Ap
c 24	34.8	25.8	6591	8	US-08-781-986A-3114	Sequence 3114, Ap
c 25	34.4	25.5	214	9	US-09-815-242-3628	Sequence 3628, Ap
c 26	34.4	25.5	400	8	US-08-781-986A-3650	Sequence 3650, Ap
c 27	34.4	25.5	400	8	US-08-781-986A-3736	Sequence 3736, Ap
c 28	34.4	25.5	449	8	US-08-781-986A-3687	Sequence 3687, Ap
c 29	34.4	25.5	619	8	US-08-781-986A-3571	Sequence 3571, Ap
c 30	34	25.2	687	8	US-08-781-986A-608	Sequence 608, App
c 31	33	24.4	3309400	10	US-09-738-626-1	Sequence 1, Appli
c 32	32.2	23.9	11103	12	US-10-056-405-23	Sequence 23, Appl
c 33	32.2	23.9	11103	14	US-10-094-240-23	Sequence 23, Appl
c 34	31.2	23.1	7690	12	US-10-311-455-1096	Sequence 1096, Ap
c 35	30.4	22.5	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 36	29.6	21.9	4792	10	US-09-863-040-5	Sequence 5, Appli
c 37	28.8	21.3	816	14	US-10-156-761-6550	Sequence 1, Appli
c 38	28.8	21.3	9025608	14	US-10-156-761-1	Sequence 3, Appli
c 39	28.4	21.0	585	10	US-09-954-973-3	Sequence 199163,
c 40	28.4	21.0	611	13	US-10-027-632-199163	Sequence 199164,
c 41	28.4	21.0	611	13	US-10-027-632-199164	Sequence 1, Appli
c 42	28.2	20.9	43804	9	US-09-970-711-1	Sequence 5266, Ap
c 43	27.6	20.4	786	14	US-10-156-761-5266	Sequence 251155,
c 44	27.6	20.4	1058	13	US-10-027-632-251155	Sequence 251156,
c 45	27.6	20.4	1058	13	US-10-027-632-251156	

ALIGNMENTS

RESULT 1

US-09-974-974-5
; Sequence 5, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 5
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal promoter sequence
US-09-974-974-5

Query Match 61.3%; Score 82.8; DB 11; Length 88;
Best Local Similarity 97.7%; Pred. No. 5.3e-20;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGUGUGUAGUGGUUACAGUCGCGUACACGCGAAAGGCCCGG 60

Db 1 ACCGUGGUUCCGUGUGUAGUGGUUACAGUCGCGUACACGCGAAAGGCCCGG 60

QY 61 UUCGAAACCGGCACUACAAACACAA 86

Db 61 UUCGAAACCGGCACUACAAACACAA 86

RESULT 2

Sat Sep 13 18:35:15 2003

us-09-763-590-1.rni

Page 9

Search completed: September 13, 2003, 08:05:55
Job time : 67.4891 secs

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; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 947:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1586RP
;
US-08-998-416-947

Query Match 23.4%; Score 31.6; DB 3; Length 702;
Best Local Similarity 47.1%; Pred. No. 0.062;
Matches 33; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 4 GUUGUUUCCGAGUGAGUGGUAUACACGUGCCUAACGCGAAGGUCGCCCGGUC 63
Db 529 GTTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTC 470

QY 64 GAAACCGGGC 73
Db 469 GATCCTGGGC 460

RESULT 14
US-07-789-915A-7/c
; Sequence 7, Application US/07789915A
; Patent No. 5212058
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,915A
; FILING DATE: 19911108
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-5091AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4887 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1278..4013

US-08-998-416-947

Query Match 23.4%; Score 31.6; DB 3; Length 702;
Best Local Similarity 47.1%; Pred. No. 0.062;
Matches 33; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 4 GUUGUUUCCGAGUGAGUGGUAUACACGUGCCUAACGCGAAGGUCGCCCGGUC 63
Db 529 GTTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTC 470

QY 64 GAAACCGGGC 73
Db 469 GATCCTGGGC 460

RESULT 15
US-08-005-002C-7/c
; Sequence 7, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/005,002C
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,915
; FILING DATE: 08-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: MIT-5091AAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0558
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4887 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1278..4013

US-08-005-002C-7

Query Match 22.7%; Score 30.6; DB 1; Length 4887;
Best Local Similarity 46.4%; Pred. No. 0.27;
Matches 32; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 5 UUGGUUCCGAGUGAGUGGUAUACACGUGCCUAACGCGAAGGUCGCCCGGUCG 64
Db 4247 TTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTCG 4188

QY 65 AAACCGGGC 73
Db 4187 ATCCTGGGC 4179

Query Match 22.7%; Score 30.6; DB 1; Length 4887;
Best Local Similarity 46.4%; Pred. No. 0.27;
Matches 32; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 5 UUGGUUCCGAGUGAGUGGUAUACACGUGCCUAACGCGAAGGUCGCCCGGUCG 64
Db 4247 TTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTCG 4188

QY 65 AAACCGGGC 73
Db 4187 ATCCTGGGC 4179
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OTHER INFORMATION:	n=a or c or g or t	
NAME/KEY:	misc_feature	
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NAME/KEY:	misc_feature	
LOCATION:	(4650001)..(4800000)	
OTHER INFORMATION:	n=a or c or g or t	
NAME/KEY:	misc_feature	
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OTHER INFORMATION:	n=a or c or g or t	
NAME/KEY:	misc_feature	
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NAME/KEY:	misc_feature	
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OTHER INFORMATION:	n=a or c or g or t	
NAME/KEY:	misc_feature	
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NAME/KEY:	misc_feature	
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OTHER INFORMATION:	n=a or c or g or t	
NAME/KEY:	misc_feature	
LOCATION:	(7650001)..(7800000)	


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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512.861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293.520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337.608
; FILING DATE: August 19, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-6

Query Match      29.5%; Score 39.8; DB 3; Length 171;
Best Local Similarity 86.3%; Pred. No. 4.6e-05;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGACGCGGAAACGGU 132
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Db      86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGACGCGGAAACGGU 136

RESULT 7
US-08-512-861A-10
; Sequence 10, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512.861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293.520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337.608
; FILING DATE: August 19, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-4

Query Match      28.4%; Score 38.4; DB 3; Length 146;
Best Local Similarity 97.5%; Pred. No. 0.00014;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGACG 121
      |||||||
Db      86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGAGG 125
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; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-10

Query Match      29.5%; Score 39.8; DB 3; Length 171;
Best Local Similarity 86.3%; Pred. No. 4.6e-05;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGACGCGGAAACGGU 132
      |||||||
Db      86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGACGCGGAAACGGU 136

RESULT 8
US-08-512-861A-4
; Sequence 4, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512.861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293.520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337.608
; FILING DATE: August 19, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-4

Query Match      28.4%; Score 38.4; DB 3; Length 146;
Best Local Similarity 97.5%; Pred. No. 0.00014;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGACG 121
      |||||||
Db      86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCGAGG 125
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Query Match 51.7%; Score 69.8; DB 3; Length 132;
 Best Local Similarity 72.6%; Pred. No. 9.4e-16;
 Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;
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 Db 11 ACCGTGGTTCCTAGTGTAGTGTATCAGTTCGCTCACACGGGACGGTCCCGG 70
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 QY 61 UUCGAAACCGGCG 73
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 Db 71 TTCGAAACCGGCG 83

RESULT 4
 PCT-US94-05700-17
 ; Sequence 17, Application PC/TUS9405700
 ; GENERAL INFORMATION:
 ; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 ; TITLE OF INVENTION: RIBOZYME GENE THERAPY FOR HIV INFECTION AND AIDS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ROBBINS, BERLINER & CARSON
 ; STREET: 201 NORTH FIGUEROA STREET
 ; CITY: LOS ANGELES
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 90012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/05700
 ; FILING DATE: 17 MAY 1994
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BERLINER, ROBERT
 ; REGISTRATION NUMBER: 20,121
 ; REFERENCE/DOCKET NUMBER: 5555-209
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 213-977-1001
 ; TELEFAX: 213-977-1003
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 133 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 97
 ; OTHER INFORMATION: /note= "w" = INTERNAL NUCLEOTIDE
 ; OTHER INFORMATION: SEQUENCE"

PCT-US94-05700-17
 Query Match 51.7%; Score 69.8; DB 5; Length 133;
 Best Local Similarity 72.6%; Pred. No. 9.4e-16;
 Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;
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 Db 11 ACCGTGGTTCCTAGTGTAGTGTATCAGTTCGCTCACACGGGACGGTCCCGG 70
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 61 UUCGAAACCGGCG 73
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 71 TTCGAAACCGGCG 83

RESULT 5
 US-08-512-861A-14
 ; Sequence 14, Application US/08512861A

; Patent No. 6146886
 ; GENERAL INFORMATION:
 ; APPLICANT: James D. Thompson
 ; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
 ; EXPRESSION OF THERAPEUTIC RNAs
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/512,861A
 ; FILING DATE: August 8, 1995
 ; PRIOR APPLICATION DATA: Two
 ; APPLICATION NUMBER: 08/293,520
 ; FILING DATE: August 19, 1994
 ; APPLICATION NUMBER: 08/337,608
 ; FILING DATE: No. 6146886ember 10, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 215/154
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 167
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-512-861A-14
 Query Match 31.9%; Score 43; DB 3; Length 167;
 Best Local Similarity 90.2%; Pred. No. 3.4e-06;
 Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 78 CAAACACACACUGAGUGAGGACGCGGAAAGGUCGCGGAAAGGCGGCGGAAA 128
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 Db 101 CAAACACACACUGAGUGAGGACGCGGAAAGGUCGCGGAAAGGCGGCGGAAA 151
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 RESULT 6
 US-08-512-861A-6
 ; Sequence 6, Application US/08512861A
 ; Patent No. 6146886
 ; GENERAL INFORMATION:
 ; APPLICANT: James D. Thompson
 ; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
 ; EXPRESSION OF THERAPEUTIC RNAs
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage

OTHER INFORMATION: /note= "insertion location of
foreign gene in pol III
OTHER INFORMATION: transcription cassette in
OTHER INFORMATION: vector pMT"
US-08-245-742A-17

Query Match 51.7%; Score 69.8; DB 1; Length 132;
Best Local Similarity 72.6%; Pred. No. 9.4e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

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Db 11 ACCGTGGTTCCGAGTAGTGTATCAGTTCGCTCACACGGGACGGTCCCGG 70

QY 61 UUCGAAACGGGC 73

Db 71 TTCGAAACGGGC 83

RESULT 2

US-08-465-483-17

Sequence 17, Application US/08465483

Patent No. 5811275

GENERAL INFORMATION:

APPLICANT: Wong-Staal, Flossie

APPLICANT: Yu, Mang

APPLICANT: Yamada, Osamu

APPLICANT: Ojwang, Joshua O.

APPLICANT: Leavitt, Mark

APPLICANT: Ho, Anthony

TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection

TITLE OF INVENTION: and AIDS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Tower

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,483

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/062,465

FILING DATE: 17-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/245,742

FILING DATE: 17-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 2307E-567-11

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: (96^97)

OTHER INFORMATION: /note= "insertion location of

OTHER INFORMATION: foreign gene in pol III
OTHER INFORMATION: transcription cassette in
OTHER INFORMATION: vector pMT"
US-08-465-483-17

Query Match 51.7%; Score 69.8; DB 1; Length 132;
Best Local Similarity 72.6%; Pred. No. 9.4e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUUGCCGAGUGGUGUUAUCACGUGGCUAACACGCGGAAAGGUCGCCGG 60

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QY 61 UUCGAAACGGGC 73

Db 71 TTCGAAACGGGC 83

RESULT 3

US-08-876-996-17

Sequence 17, Application US/08876996

Patent No. 6132962

GENERAL INFORMATION:

APPLICANT: Wong-Staal, Flossie

APPLICANT: Yu, Mang

APPLICANT: Yamada, Osamu

APPLICANT: Ojwang, Joshua O.

APPLICANT: Leavitt, Mark

APPLICANT: Ho, Anthony

TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection

TITLE OF INVENTION: and AIDS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Tower

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/876,996

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,742

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 2307E-567-10

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: (96^97)

OTHER INFORMATION: /note= "insertion location of

foreign gene in pol III

OTHER INFORMATION: transcription cassette in

OTHER INFORMATION: vector pMT"

US-08-876-996-17

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Perfect score: 135

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	69.8	51.7	132	3	US-08-876-996-17 Sequence 17, Appl
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5	43.3	31.9	137	3	US-08-512-861A-14 Sequence 14, Appl
6	39.8	29.5	171	3	US-08-512-861A-6 Sequence 6, Appl
7	39.8	29.5	171	3	US-08-512-861A-10 Sequence 10, Appl
8	38.4	28.4	146	3	US-08-512-861A-4 Sequence 4, Appl
9	38.4	28.4	146	3	US-08-512-861A-8 Sequence 8, Appl
10	34.4	25.5	186	4	US-09-107-532A-488 Sequence 488, App
11	34.4	25.5	1483	1	US-08-270-076A-2 Sequence 2, Appl
12	32.6	24.1	1230025	4	US-09-198-452A-1 Sequence 1, Appl
13	31.6	23.4	782	3	US-08-998-416-947 Sequence 947, App
14	30.6	22.7	4887	1	US-07-789-915A-7 Sequence 7, Appl
15	30.6	22.7	4887	1	US-08-005-002C-7 Sequence 7, Appl
16	30.6	22.7	4887	1	US-08-487-203A-7 Sequence 7, Appl
17	29.8	22.1	1664976	4	US-08-916-421B-1 Sequence 1, Appl
18	29.6	21.9	648	3	US-08-998-416-111 Sequence 11, App
19	29.6	21.9	4792	3	US-08-189-462-5 Sequence 5, Appl
20	29.4	21.8	729	3	US-08-998-416-607 Sequence 607, App
21	29.4	21.8	1664976	4	US-08-916-421B-1 Sequence 1, Appl
22	28.8	21.3	1284	4	US-09-252-991A-6826 Sequence 6826, Ap
23	28.8	21.3	1305	4	US-09-252-991A-6918 Sequence 6918, Ap
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26	28	20.7	21338	4	US-08-961-527-1 Sequence 20, Appl
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32	27	20.0	61663	4	US-08-453-702B-62	Sequence 62, Appl
33	26.6	19.7	724	1	US-08-599-252-98	Sequence 98, Appl
34	26.6	19.7	724	5	PCT-US96-06352-98	Sequence 98, Appl
35	26.6	19.7	724	5	PCT-US96-06583-98	Sequence 98, Appl
36	26.2	19.4	189	4	US-09-328-352-1239	Sequence 1239, Ap
37	26.2	19.4	724	3	US-08-961-083-45	Sequence 45, Appl
38	26.2	19.4	724	4	US-09-536-784-45	Sequence 45, Appl
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40	26	19.3	34063	4	US-09-453-702B-96	Sequence 96, Appl
41	26	19.3	49795	4	US-09-453-702B-60	Sequence 60, Appl
42	25.8	19.1	2271	4	US-09-438-268-3	Sequence 3, Appli
43	25.8	19.1	49272	1	US-08-614-770A-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 17, Application US/08245742A
; Patent No. 5670361
; GENERAL INFORMATION:
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Yu, Mang
; APPLICANT: Yamada, Osamu
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Leavitt, Mark
; APPLICANT: Ho, Anthony
; TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
; TITLE OF INVENTION: and AIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94103-1492

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,742A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,465
; FILING DATE: 17-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 2307E-567-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: (96-97)

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PD           17-JUL-2001
PF           02-NOV-2000 JP 2000336082
PI           KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI PI
            KAWASAKI
PC
C12N15/09,A61K31/7105,A61K31/711,A61K38/00,A61K48/00,A61P31/12, PC
A61P43/00,
PC C12N9/22,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00, PC
A61K37/02
CC Description of Artificial Sequence: the sequence encoding CC
   tRNAval-TAR GUU
CC Rz-CTE
CC Other information: the sequence of nucleotide numbers 1-91 is
CC of tRNAval
CC with 3'-modification
CC Other information: the sequence of nucleotide numbers 92-131
CC is of TAR GUU
CC Rz
CC Other information: the sequence of nucleotide numbers 132-137
CC is of a
CC KpnI-recognition site
CC Other information: the sequence of nucleotide numbers 138-309
CC is of CTE
CC Other information: the sequence of nucleotide numbers 310-315
CC is of an
CC EcoRV-recognition site
CC Other information: the sequence of nucleotide numbers 316-320
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CC terminator
CC Key
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/organism="synthetic construct"
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Best Local Similarity 69.7%; Pred. NO. 7.5e-15;
Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;
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 DEFINITION Slidable functional chimeric molecule.
 ACCESSION BD015617
 VERSION BD015617.1 GI:22556754
 KEYWORDS JP 2001190282-A/10.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 151)
 AUTHORS Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
 TITLE Slidable functional chimeric molecule
 JOURNAL Patent: JP 2001190282-A 10 17-JUL-2001;
 DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
 SCIENCE AND MANABU NAKAJIMA TECHNOLOGY, KAZUNARI TAIRA
 COMMENT OS Artificial Sequence
 PN JP 2001190282-A/10
 PD 17-JUL-2001
 PF 02-NOV-2000 JP 2000336082
 PI KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI PI
 KAWASAKI
 PC C12N15/09,A61K31/7105,A61K31/711,A61K38/00,A61K48/00,A61P31/12,PC
 A61P43/00,
 PC C12N9/22,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,PC
 A61K37/02
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 CC of RNAval-linked
 CC TAR GUU RZ
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 CC with 3'-modification
 CC Other information: the sequence of nucleotide numbers 92-131
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 CC Other information: the sequence of nucleotide numbers 132-137
 CC is of a
 CC KpnI-recognition site
 CC Other information: the sequence of nucleotide numbers 138-140
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 CC linker
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 Query Match 62.7%; Score 84.6; DB 6; Length 151;
 Best Local Similarity 69.7%; Pred. No. 7.5e-15;
 Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;

QY 1 ACCGUGUUCUCCGAGUGAGUGGUAUACACGUCUACACGCGAAAGGUCGCCGG 60
 DB 1 ACCGTTGGTTCCGTTAGTGTAGTTATCAGTTCGCTTACACGCGAAAGGTCGCCGG 60
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 DB 61 TTCGAAACCGGCGACTACAAAACCACTTTATCTGGTC 99
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 DEFINITION Sequence 11 from Patent EP1097993.
 ACCESSION AX138450
 VERSION AX138450.1 GI:14274346
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
 TITLE Functional ribozyme chimeric molecules capable of sliding
 JOURNAL Patent: EP 1097993-A 11 09-MAY-2001;
 Secretary of Agency of Industrial Science and Technology (JP);
 Taira, Kazunari (JP)
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 /db_xref='taxon:32630'
 /note='the sequence encoding tRNAval-TAR GUU RZ-CTE-Other
 information: the sequence of nucleotide numbers 1-91 is of
 tRNAval with 3'-modification.-Other information: the
 sequence of nucleotide numbers 92-131 is of TAR GUU
 RZ.-Other information: the sequence of nucleotide numbers
 132-137 is of a KpnI-recognition site.-Other information:
 the sequence of nucleotide numbers 138-309 is of
 CTE.-Other information: the sequence of nucleotide numbers
 310-315 is of an EcoRV-recognition site.-Other
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 of a terminator.'
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 Query Match 62.7%; Score 84.6; DB 6; Length 320;
 Best Local Similarity 69.7%; Pred. No. 7.5e-15;
 Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ACCGUGUUCUCCGAGUGAGUGGUAUACACGUCUACACGCGAAAGGUCGCCGG 60
 DB 1 ACCGTTGGTTCCGTTAGTGTAGTTATCAGTTCGCTTACACGCGAAAGGTCGCCGG 60
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 DEFINITION Slidable functional chimeric molecule.
 ACCESSION BD015618
 VERSION BD015618.1 GI:22556755
 KEYWORDS JP 2001190282-A/11.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 320)
 AUTHORS Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
 TITLE Slidable functional chimeric molecule
 JOURNAL Patent: JP 2001190282-A 11 17-JUL-2001;
 DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
 SCIENCE AND MANABU NAKAJIMA TECHNOLOGY, KAZUNARI TAIRA

RESULT 10
 LOCUS BD143601 137 bp RNA linear PAT 17-JAN-2003
 DEFINITION Method of selecting high-function nucleic acid molecule in cell.
 ACCESSION BD143601
 VERSION BD143601.1 GI:27849359
 KEYWORDS JP 2002125685-A/2.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 137)
 AUTHORS Taira, K. and Sano, M.
 TITLE Method of selecting high-function nucleic acid molecule in cell
 JOURNAL DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
 SCIENCE AND HIROSHI YATSUSHI, TECHNOLOGY, KAZUNARI TAIRA
 COMMENT OS Artificial Sequence
 PN JP 2002125685-A/2
 PD 08-MAY-2002
 PF 30-OCT-2000 JP 2000331347
 PI KAZUNARI TAIRA, MASAYUKI SANO
 PC C12N15/09, C12N9/00, C12Q1/02, C12Q1/25, C12Q1/68, C12M15/00 CC
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 QY 121 GUCGGAACCGGUU 135
 Db 121 AACGTGATGTTT 135

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 ACCESSION AB080619
 VERSION AB080619.1 GI:22531652
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Tachi, C., Nakamura, K., Horii, T., Murata, C., Nishimura, S.,
 Nishino, K., Nakayama, A. and Taira, K.
 TITLE Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 153)
 AUTHORS Tachi, C.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
 Veterinary Medicine, Lab. Developmental and Reproductive

Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
 (E-mail: tachi@azabu-u.ac.jp, Tel: 81-3-3997-2757)
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 QY 121 GUCGGAACCGGUU 133
 Db 121 AAGCAACTGGGT 133

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 VERSION AX138449.1 GI:14274345
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Taira, K., Warashina, M., Kuwabara, T. and Kawasaki, H.
 TITLE Functional ribozyme chimeric molecules capable of sliding
 JOURNAL Patent: EP 1097993-A 10 09-MAY-2001;
 Secretary of Agency of Industrial Science and Technology (JP);
 Taira, Kazunari (JP)
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 1-91 is of tRNAval with 3'-modification. Other
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 nucleotide numbers 132-137 is of a KpnI-recognition
 site. Other information: the sequence of nucleotide
 numbers 138-140 is of a linker. Other information: the
 sequence of nucleotide numbers 141-146 is of an
 EcoRV-recognition site. Other information: the sequence of
 nucleotide numbers 147-151 is of a terminator."
 BASE COUNT 38 a 39 c 38 g 36 t
 ORIGIN

Query Match 62.7%; Score 84.6; DB 6; Length 151;
 Best Local Similarity 69.7%; Pred. No. 7.5e-15;
 Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;

PN	JP 200069972-A/12
PD	07-MAR-2000
Pf	31-AUG-1998 JP 1998244755
PR	KAZUNARI TABIRA, ATSUSHI OKAWA, SHIORI OZEKI
PI	C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
PC	Key Location/Qualifiers
FH	1. 109
FT	/organism='Artificial Sequence'
FEATURES	
source	Location/Qualifiers
	. . 109
	/organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
BASE COUNT	18 A 29 C 30 G 32 T
ORIGIN	
Query Match	63.3%; Score 85.4; DB 6; Length 109;
Best Local Similarity	86.2%; Pred. No. 4.3e-15;
Matches	75; Conservative %; Mismatches 1; Indels 0; Gaps 0;
QY	49 AAAGGUCGCCGUUCCGAACCGGGCACACACAACCAACACACACUCAGUAGGACGCAGAAGGUC 108 ::: ::: ::: ::: ::: ::: ::: ::
Dd	109 AAAGTCCCCGTTCGAAACCGGGCCTACTCAAACACACACTCATATGAGGACCAGAAAGGAC 50
QY	109 CGAACGGGCACGUGCAGACGGUUU 135 ::: ::: ::: ::: ::: ::: ::: ::
Dd	49 CAACACGGGCACGTCGGAACGGTTT 23
RESULT 9	
LOCUS	AX429079 linear PAT 21-JUN-2002
DEFINITION	Sequence 2 from Patent EP1201751.
ACCESSION	AX429079
VERSION	AX429079.1 GI:21540419
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Taira,K. and Sano,M.
TITLE	Method for selecting highly functional nucleic acid molecules within cells
JOURNAL	Patent: EP 1201751-A 2 02-MAY-2002; National Institute of Advanced Industrial Science and Technology (Jp)
FEATURES	
source	Location/Qualifiers
	. . 137
	/organism="synthetic construct"
	/mol_type="mRNA"
	/db_xref="taxon:32630"
	/note="Sequence of tRNA-Luc GUA Rz"
BASE COUNT	33 A 34 C 34 G 36 T
ORIGIN	
Query Match	63.3%; Score 85.4; DB 6; Length 137;
Best Local Similarity	58.5%; Pred. No. 4.3e-15;
Matches	79; Conservative 25; Mismatches 31; Indels 0; Gaps 0;
QY	1 ACCGTRUGGUUCCGAGUGAGUGGUUACUACGUCGUACACGCGAAGGUCGCCGG 60 ::: ::: ::: ::: ::: ::: ::: ::
Dd	1 ACCGTGTGTTTTCCGTAGTAGTGTTACAGTTCGCTTAACACGCGAAGGTCGCCGG 60
QY	61 UUCGAAAACCGGGCACACAAAAACACACACUCAGUAGGACCGAAAGGUCGCAACGGGCAC 120 ::: ::: ::: ::: ::: ::: ::: ::: ::
Dd	61 TTCGAAAACCGGGCCTACTAAAAACCAACTATTTCGCGCTGATGAGGCGCAAGGCGCA 120
QY	121 GUCCGAAACGGUUUU 135 : :
Dd	121 AACGTGATGTTTTT 135


```

COMMENT      OS      Artificial Sequence
FN          JP 2000069972-A/1
PD          07-MAR-2000
PR          31-AUG-1998 JP 1998244755
PI          KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI
PC          C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
FH          Key      Location/Qualifiers
FT          source    1..136
                     /organism="Artificial Sequence".
FEATURES
  source      Location/Qualifiers
               1..136
               /organism="synthetic construct"
               /mol_type="genomic RNA"
               /db_xref="taxon:32630" 28 t
BASE COUNT   36 a 35 c 37 g 28 t
ORIGIN
Query Match 100.0%; Score 135; DB 6; Length 136;
Best Local Similarity 80.0%; Pred. No. 5e-30;
Matches 108; Conservative 27; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGUUGUUCGUGAGUGAGUGGUUAUCACGUCUACACGCGGAAAGGUCCCGG 60
Db 1 ACCGTTGGTTCCGTAGTGTAGTGTATCAGCTTCGCTACACGCGGAAAGGTCGCCGG 60
QY 61 UUGGAAACCGGGCACUACAAACACACACACUGAUGAGGACCGGAAAGGUCCGAAACGGGCAC 120
Db 61 TTCGAAACCGGGCAGTACAAACACACACACACTGATGAGGACCGGAAAGGTCGGAACGGGCAC 120
QY 121 GUCGGAACCGGUUUU 135
Db 121 GTCGGAACCGGTTT 135

RESULT 2
E33204      142 bp RNA linear PAT 31-JAN-2002
LOCUS       Expression system for functional nucleic acid transcription.
DEFINITION  E33204
ACCESSION   E33204
VERSION     E33204.1 GI:18623998
KEYWORDS    JP 2000069972-A/2.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 142)
            Tabira,K., Okawa,A. and Ozeki,S.
            Expression system for functional nucleic acid transcription
            Patent: JP 2000069972-A 2 07-MAR-2000;
            AGENCY OF IND. SCIENCE & TECHNOL
OS          Artificial Sequence
PN          JP 2000069972-A/2
PD          07-MAR-2000
PR          31-AUG-1998 JP 1998244755
PI          KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI
PC          C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
FH          Key      Location/Qualifiers
FT          source    1..142
                     /organism="Artificial Sequence".
FEATURES
  source      Location/Qualifiers
               1..142
               /organism="synthetic construct"
               /mol_type="genomic RNA"
               /db_xref="taxon:32630" 28 t
BASE COUNT   39 a 38 c 37 g 28 t
ORIGIN
Query Match 88.1%; Score 119; DB 6; Length 142;
Best Local Similarity 76.6%; Pred. No. 3.3e-25;
Matches 108; Conservative 27; Mismatches 0; Indels 6; Gaps 1;
QY 1 ACCGUUGUUCGUGAGUGAGUGGUUAUCACGUCUACACGCGGAAAGGUCCCGG 60

```

```

Db 1 ACCGTTGGTTCCGTAGTGTAGTGTATCAGCTTCGCTACACGCGGAAAGGTCGCCGG 60
QY 61 UUGGAAACCGGGCACUACAA-----ACACACACACUGAUGAGGACCGGAAAGGUCCGAAAC 114
Db 61 TTCGAAACCGGGCAGTACAAACACACACACACACTGATGAGGACCGGAAAGGTCGGAAC 120
QY 115 GGGCAGUCGCGGAACGGUUU 135
Db 121 GGCACGTCGGAACCGGTTT 141

RESULT 3
BD174680    175 bp DNA linear PAT 18-MAR-2003
LOCUS       Ribozyme expression system.
DEFINITION  BD174680
ACCESSION   BD174680
VERSION     BD174680.1 GI:29120370
KEYWORDS    JP 2002262880-A/6.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 175)
            Takebe,X. and Okawa,J.
            Ribozyme expression system
            Patent: JP 2002262880-A 6 17-SEP-2002;
            DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
            YUTAKA TAKEBE,JUN OKAWA
OS          Artificial Sequence
PN          JP 2002262880-A/6
PD          17-SEP-2002
PR          09-MAR-2001 JP 2001067253
PI          YUTAKA TAKEBE,JUN OKAWA
PC          C12N15/09,A61K31/71,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
            C12N9/00,
            C12N15/00,C12N5/00
CC          Description of Artificial Sequence: the
            nucleotide sequence of
            CC ribozyme
            CC expressing cassette of the invention
            FH Key      Location/Qualifiers
            FT source    1..175
                     /organism="Artificial Sequence".
FEATURES
  source      Location/Qualifiers
               1..175
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630" 46 t
BASE COUNT   48 a 40 c 41 g 46 t
ORIGIN
Query Match 67.6%; Score 91.2; DB 6; Length 175;
Best Local Similarity 69.2%; Pred. No. 7.7e-17;
Matches 101; Conservative 26; Mismatches 8; Indels 11; Gaps 2;
QY 1 ACCGUUGUUCGUGAGUGAGUGGUUAUCACGUCUACACGCGGAAAGGTCGCCGG 60
Db 29 ACCGTTGGTTCCGTAGTGTAGTGTATCAGCTTCGCTACACGCGGAAAGGTCGCCGG 88
QY 61 UUGGAAACCGGGCACUACAAACAC-----AACACUGAUGAGGACCGGAAAGGUCCG 110
Db 89 TTCGAAACCGGGCAGTACAAACACACACCATAGATTGCTGATGAGGACCGGAAAGGTCG 148
QY 111 AACACGGGACGUCGGAACGGUUU 135
Db 149 AAATTGACACTCCGGAACCGGTTT 174

RESULT 4
BD174679    175 bp DNA linear PAT 18-MAR-2003
LOCUS       Ribozyme expression system.
DEFINITION  BD174679
ACCESSION   BD174679

```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 09:38:16 : Search time 1374.45 Seconds
(without alignments)
4018.170 Million cell updates/sec

Title: US-09-763-590-1

Perfect score: 135

Sequence: 1 accguugnuccguagu.....ggcacgucggaacgguuuu 135

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_intg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	135	100.0	136	6	E33203	E33203 Expression
2	119	88.1	142	6	E33204	E33204 Expression
3	91.2	67.6	175	6	BD174680	BD174680 Ribozyme
4	89.4	66.2	175	6	BD174679	BD174679 Ribozyme
5	87.6	64.9	153	12	AB080624	AB080624 Synthetic
6	87.4	64.7	142	6	AX138492	AX138492 Sequence
7	87.4	64.7	142	6	BD015660	BD015660 Slidable
8	85.4	63.3	109	6	E33214	E33214 Expression
9	85.4	63.3	137	6	AX429079	AX429079 Sequence
10	85.4	63.3	137	6	BD143601	BD143601 Method of
11	85	63.0	153	12	AB080619	AB080619 Synthetic
12	84.6	62.7	151	6	AX138449	AX138449 Sequence
13	84.6	62.7	151	6	BD015617	BD015617 Slidable
14	84.6	62.7	320	6	AX138450	AX138450 Sequence
15	84.6	62.7	320	6	BD015618	BD015618 Slidable
16	84.4	62.5	153	12	AB080622	AB080622 Synthetic
17	83.8	62.1	153	12	AB080620	AB080620 Synthetic
18	83.8	62.1	153	12	AB080621	AB080621 Synthetic
19	83.8	62.1	153	12	AB080623	AB080623 Synthetic
20	82.8	61.3	88	6	AX453846	AX453846 Sequence
21	82.8	61.3	88	6	BD143502	BD143502 Nucleic a
22	82.8	61.3	88	6	BD182356	BD182356 Novel max
23	82.8	61.3	100	6	E47174	E47174 Method for
24	82.8	61.3	117	6	BD174675	BD174675 Ribozyme
25	82.8	61.3	138	6	AX453858	AX453858 Sequence
26	82.8	61.3	141	6	AX138491	AX138491 Sequence
27	82.8	61.3	141	6	BD015659	BD015659 Slidable
28	82.8	61.3	142	6	AX138488	AX138488 Sequence
29	82.8	61.3	142	6	AX138489	AX138489 Sequence
30	82.8	61.3	142	6	AX138490	AX138490 Sequence
31	82.8	61.3	142	6	BD015656	BD015656 Slidable
32	82.8	61.3	142	6	BD015657	BD015657 Slidable
33	82.8	61.3	142	6	BD015658	BD015658 Slidable
34	78	57.8	128	6	E33205	E33205 Expression
35	73.4	54.4	149	6	E33207	E33207 Expression
36	73	54.1	95	6	AX138447	AX138447 Sequence
37	73	54.1	95	6	BD015615	BD015615 Slidable
38	73	54.1	95	6	E33206	E33206 Expression
39	73	54.1	183	11	G31283	G31283 sy905gl-L H
40	73	54.1	1396	9	HSMHTV1A	M15782 Human Htv1
41	73	54.1	139904	9	HS97D16	AL009179 Human DNA
42	71.2	52.7	202559	10	AL645849	AL645849 Mouse DNA
43	71	52.6	216206	2	AC135042	AC135042 Rattus no
44	71	52.6	296028	2	AC115261	AC115261 Rattus no
45	69.8	51.7	132	6	AR041184	AR041184 Sequence

ALIGNMENTS

RESULT 1	E33203	136 bp	RNA	linear	PAT 31-JAN-2002
E33203	Expression system for functional nucleic acid transcription.				
LOCUS	E33203				
DEFINITION	E33203				
ACCESSION	E33203.1	GI:18623997			
VERSION	E33203.1	GI:18623997			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences				
REFERENCE	1 (bases 1 to 136)				
AUTHORS	Tabira,K., Okawa,A. and Ozeki,S.				
TITLE	Expression system for functional nucleic acid transcription				
JOURNAL	Patent: JP 2000069972-A 1 07-MAR-2000;				
	AGENCY OF IND SCIENCE & TECHNOL				


```

XX 09-MAR-2001; 2001JP-0067253.
XX PF
XX 09-MAR-2001; 2001JP-0067253.
XX PR
XX (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX PA
XX (TAKE/) TAKEBE Y.
XX PA
XX (OKAW/) OKAWA J.
XX PS
XX WPI; 2003-132124/13.
XX DR
XX Ribozyme expression cassette, useful for preparing a cell insensitive
XX PT to HIV and for inhibiting growth of HIV, comprises a tetracyclin
XX PT operator, at least one promoter and a sequence encoding a ribozyme
XX PT successively from the upstream side -
XX PS
XX Claim 6; Page 15; 27pp; Japanese.
XX PS
XX The present invention relates to a ribozyme expression cassette
XX CC comprising a tetracyclin operator, at least one promoter and a DNA
XX CC sequence encoding a ribozyme successively from the 5' end. The
XX CC tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from
XX CC the transcription initiating site of the promoter. The expression
XX CC cassette is useful in a method for preparing a cell having no sensitivity
XX CC to HIV, and for inhibiting the growth of HIV. To illustrate the
XX CC invention, a tet O1-human tRNAVal promoter cassette was constructed,
XX CC using the present sequence.
XX CC
XX Sequence 117 BP; 31 A; 28 C; 26 G; 32 T; 0 other;
XX SQ
Query Match 61.3%; Score 82.8; DB 25; Length 117;
Best Local Similarity 75.6%; Pred. No. 5e-19;
Matches 65; Conservative 19; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACCGUUGGUUCCGUGAGUGGUUACGUCGUAACACGCGAAGGUCGCCGG 60
DB 29 ACCGTGGTTCGGTAGTGTAGTGTATCATCGTTCGCTACACGCGAAGGTCGCCGG 88
QY 61 UUCGAAACCGGGCAGCUCACAAACACAA 86
DB 89 TTCGAAACCGGGCAGCAGTACAAACACCA 114
RESULT 15
AAL40467
ID AAL40467 standard; tRNA; 138 BP.
XX AC
XX AAL40467;
XX DT
XX 19-SEP-2002 (first entry)
XX XX
XX Maxizyme related tRNA-val T-MzL sequence.
XX XX
XX Enzyme; modifiable RNA cleavage activity; maxizyme-constituting RNA;
XX KW trans maxizyme; tRNA-val T-MzL; ss.
XX XX
XX Unidentified.
XX PH
XX Key Location/Qualifiers
XX FT misc_binding 4..11
XX FT /tag= a
XX FT /bound_moiety= "tRNA-val_T-MzL"
XX FT /note= "Forms a double-stranded region with nucleotides
XX FT 88-81 of itself"
XX FT misc_binding 14..19
XX FT /tag= b
XX FT /bound_moiety= "tRNA-val_T-MzL"
XX FT /note= "Forms a double-stranded region with nucleotides
XX FT 78-73 of itself"
XX FT stem_loop 22..32
XX FT /tag= c
XX FT stem_loop 34..50
XX FT /tag= d

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```

FT stem_loop 56..72
FT /tag= e
FT misc_binding 73..78
FT /tag= f
FT /bound_moiety= "tRNA-val_T-MzL"
FT /note= "Forms a double-stranded region with nucleotides
FT 19-14 of itself"
FT misc_binding 81..88
FT /tag= g
FT /bound_moiety= "tRNA-val_T-MzL"
FT /note= "Forms a double-stranded region with nucleotides
FT 11-4 of itself"
FT stem_loop 95..107
FT /tag= h
FT stem_loop 111..128
FT /tag= i
XX PN
XX JP2002119283-A.
XX PD
XX 23-APR-2002.
XX PF
XX 13-OCT-2000; 2000JP-0313320.
XX PR
XX 13-OCT-2000; 2000JP-0313320.
XX XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
XX DR
XX WPI; 2002-483792/52.
XX XX
XX A nucleic acid enzyme which has selective and effective eradicating
XX PT activity towards harmful cells by acquiring cleavage activity of a
XX PT specific target RNA by recognition of the other RNA molecule -
XX PS
XX Disclosure; Fig 7; 17pp; Japanese.
XX CC
XX The invention relates to a nucleic acid enzyme with modifiable RNA
XX CC cleavage activity. More specifically the invention relates to a nucleic
XX CC acid enzyme, trans maxizyme, which has selective and effective
XX CC eradicating activity towards harmful cells by acquiring cleavage activity
XX CC of a specific target RNA by recognition of the other RNA molecule. The
XX CC enzyme of the invention is useful for cleaving target RNA and is useful
XX CC in treating diseases caused by the target RNA. This polynucleotide
XX CC sequence represents the tRNA-val T-MzL sequence related to the maxizyme
XX CC enzyme of the invention.
XX SQ
Sequence 138 BP; 31 A; 38 C; 32 G; 37 U; 0 other;

```

```

Query Match 61.3%; Score 82.8; DB 24; Length 138;
Best Local Similarity 97.7%; Pred. No. 5.2e-19;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1 ACCGUUGGUUCCGUGAGUGGUUACGUCGUAACACGCGAAGGUCGCCGG 60
DB 1 ACCGUUGGUUCCGUGAGUGGUUACGUCGUAACACGCGAAGGUCGCCGG 60
QY 61 UUCGAAACCGGGCAGCUCACAAACACAA 86
DB 61 UUCGAAACCGGGCAGCUCACAAACACCA 86

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Search completed: September 13, 2003, 09:52:32
Job time : 198.152 secs

QY 1 ACCGUGGUGUCCGAGUAGUGGUGUUAUCAGUCCGCUAACACGCGAAAGGUCGCCGG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 ACCGUGGUGUCCGAGUAGUGGUGUUAUCAGUCCGCUAACACGCGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGGCACUACAAACACAA 86
Db |||||||||||||||||||||||||||||||

61 UUCGAAACCGGGCACUACAAACACAA 86

RESULT 12

ABX12785

ID ABX12785 standard; RNA; 88 BP.

AC ABX12785;

XX

DT 15-MAY-2003 (first entry)

XX

DE Human RNA sequence relating to novel maxizyme.

XX

KW Human; maxizyme; target mRNA; helicase activity; viral disease;

KW human immunodeficiency virus; HIV; hepatitis C; hepatitis B; cancer;

KW apoptosis-associated disease; Alzheimer's disease; Parkinson's disease;

KW autoimmune disease; inflammatory disease; genetic disorder;

KW mRNA cleavage; virucide; neurotropic; antiparkinsonian; cytostatic;

KW antiinflammatory; immunosuppressive; ss.

XX

OS Homo sapiens.

XX

PN WO200292821-A1.

XX

PD 21-NOV-2002.

XX

PF 30-APR-2002; 2002WO-JP04322.

XX

PR 01-MAY-2001; 2001JP-0134469.

XX

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX

PA (TAIS) TAISHO PHARM CO LTD.

XX

PA (GENO-) GENOFUNCTION INC.

XX

PI Taira K, Warashina T, Warashina M, Kawasaki H, Hara T, Nozawa I;

XX

XX WPI; 2003-129298/12.

DR

DX Maxizyme binding to a molecule with helicase activity for treatment of

XX

PT viral infection cancer and autoimmune disease

XX

PS Claim 11; Page 30-31; 36pp; Japanese.

XX

CC The present invention relates to a novel maxizyme that can bind to a
CC target mRNA molecule or a molecule having helicase activity. The
CC maxizyme is useful for the prevention and treatment of viral diseases
CC such as human immunodeficiency virus (HIV), hepatitis C or hepatitis B,
CC apoptosis-associated diseases such as Alzheimer's and Parkinson's
CC diseases, cancer, autoimmune diseases, inflammatory diseases and
CC genetic disorders. The maxizyme binds to and cleaves target mRNA
CC irrespective of the higher-order structure of the latter. The present
CC sequence represents a human RNA sequence relating to the present
CC invention.

XX

SQ Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;

XX

Query Match 61.3%; Score 82.8; DB 25; Length 88;

Best Local Similarity 97.7%; Pred. No. 4.6e-19;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 ACCGUGGUGUCCGAGUAGUGGUGUUAUCAGUCCGCUAACACGCGAAAGGUCGCCGG 60

Db

1 ACCGUGGUGUCCGAGUAGUGGUGUUAUCAGUCCGCUAACACGCGAAAGGUCGCCGG 60

QY

61 UUCGAAACCGGGCACUACAAACACAA 86

Db

61 UUCGAAACCGGGCACUACAAACACAA 86

PT disease, comprises region with binding affinity for molecule capable of
 PT sliding

XX Example 1; Page 13; 76pp; English.

CC The present sequence is that of a DNA cassette forming part of a
 CC ribozyme expression vector of the invention. The cassette
 CC comprises the human placental TRNAval promoter (see AAF903356), with
 CC a 3' modification, a DNA sequence corresponding to HIV-1
 CC mRNA-targeted ribozyme TAR GUD R2 (see AAF903354), and a 3'
 CC constitutive transport element (CTE, see AAF90344) derived from
 CC Mason-Pfizer monkey virus. Chimeric molecules of the invention
 CC include ribozymes such as TAR GUD R2 linked to a CTE, and
 CC expression vectors for such chimeric molecules. These are used in
 CC a claimed method to prevent or treat viral diseases, diseases
 CC associated with apoptosis or diseases associated with abnormal
 CC gene expression. They are also used in a claimed method of
 CC specifically cleaving a target nucleic acid, especially a viral
 CC gene, protooncogene or a gene associated with apoptosis. Use
 CC of the CTE facilitates cleavage of RNA previously considered
 CC refractory because of local structure.

XX Sequence 320 BP; 93 A; 79 C; 81 G; 67 T; 0 other;

Query Match 62.7%; Score 84.6; DB 22; Length 320;
 Best Local Similarity 69.7%; Pred. No. 1.6e-19;
 Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUUCGGUAGUGUAGUACACGUCGCUAACACGCGGAAAGGUCGCCGG 60

Db 1 ACCGTGTGTTCCGTAGTGTAGTGTATACGTTGCGCTAACACGCGGAAAGGTCGCCGG 60

QY 61 UUCGAAACCGGCGACUACAAACACACACACUCAGUAGAGGAC 99

Db 61 TTCGAAACCGGCGACTACAAAACCAACTTTATCTGTC 99

RESULT 10

AAZ10600
 ID AAZ10600 standard; RNA; 88 BP.

XX AAZ10600;

XX 17-NOV-1999 (first entry)

XX Nucleotide sequence of tRNA-val.

XX Nucleic acid enzyme; maxizyme; allosteric RNA-cleaving activity;
 KW RNA cleavage; chronic myeloid leukemia;
 KW Philadelphia chromosome abnormality; ss.

XX Synthetic.

XX WC9946388-A1.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-JP01187.

XX 12-MAR-1998; 98JP-0060969.

XX 30-OCT-1998; 98JP-0311098.

XX (TAIS) TAISHO PHARM CO LTD.

PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

XX Taira K, Kuwabara T, Hitoshio A;

XX WPI; 1999-551415/46.

XX Nucleic acid enzyme having allosteric RNA-cleaving activity, used for

PT treatment of chronic myeloid leukemia

XX Claim 8; Page 55; 93pp; Japanese.

XX

CC The specification describes nucleotide sequences which make up the
 CC left and right arms of a nucleic acid enzyme (maxizyme). The maxizyme
 CC has allosteric RNA-cleaving activity on a specific target RNA. The
 CC maxizyme can be used for efficient cleavage of RNA molecules at
 CC specific points, especially for the prevention and treatment of
 CC chronic myeloid leukemia and Philadelphia chromosome abnormality.
 CC The present sequence is used in the course of the invention.

XX Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;

Query Match 61.3%; Score 82.8; DB 20; Length 88;
 Best Local Similarity 97.7%; Pred. No. 4.6e-19;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUUCGGUAGUGUAGUACACGUCGCUAACACGCGGAAAGGUCGCCGG 60

Db 1 ACCGUGGUGUUCGGUAGUGUAGUACACGUCGCUAACACGCGGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGCGACUACAAACACAA 86

Db 61 UUCGAAACCGGCGACUACAAACAA 86

RESULT 11

AAZ40450

ID AAZ40450 standard; tRNA; 88 BP.

XX AAZ40450;

XX 19-SEP-2002 (first entry)

XX Maxizyme related tRNA-val promoter sequence.

XX Enzyme; modifiable RNA cleavage activity; maxizyme-constituting RNA;
 KW trans maxizyme; tRNA-val; ss.

XX Unidentified.

XX JP2002119283-A.

XX 23-APR-2002.

XX 13-OCT-2000; 2000JP-0313320.

XX 13-OCT-2000; 2000JP-0313320.

XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.

XX WPI; 2002-483792/52.

XX A nucleic acid enzyme which has selective and effective eradicating
 PT activity towards harmful cells by acquiring cleavage activity of a
 PT specific target RNA by recognition of the other RNA molecule

XX Claim 12; Page 2; 17pp; Japanese.

XX The invention relates to a nucleic acid enzyme with modifiable RNA
 CC cleavage activity. More specifically the invention relates to a nucleic
 CC acid enzyme, trans maxizyme, which has selective and effective
 CC eradicating activity towards harmful cells by acquiring cleavage activity
 CC of a specific target RNA by recognition of the other RNA molecule. The
 CC enzyme of the invention is useful for cleaving target RNA and is useful
 CC in treating diseases caused by the target RNA. This polynucleotide
 CC sequence represents the tRNA-val promoter sequence relating to the
 CC maxizyme enzyme of the invention.

XX Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;

Query Match 61.3%; Score 82.8; DB 24; Length 88;

Best Local Similarity 97.7%; Pred. No. 4.6e-19;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX Sequence 137 BP; 33 A; 34 C; 34 G; 36 U; 0 other;
 SQ Query Match 63.3%; Score 85.4; DB 24; Length 137;
 Best Local Similarity 77.0%; Pred. No. 6.5e-20;
 Matches 104; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 1 ACCGUGUUCGUGAGUGGUGUACGUGUCCUACACGCGAAGGUGCCCGG 60
 Db 1 ACCGUGUUCGUGAGUGGUGUACGUGUCCUACACGCGAAGGUGCCCGG 60
 QY 61 UUCGAAACCGGCGACUACACACACACGAGGACCGAAGGUGCCCGGCGAC 120
 Db 61 UUCGAAACCGGCGACUACACACACACGAGGACCGAAGGUGCCCGGCGA 120
 QY 121 GUCGGAACGUGUUU 135
 Db 121 AACGUGAGUGUUUU 135
 RESULT 8
 AAF90357
 ID AAF90357 standard; DNA; 151 BP.
 XX AAF90357;
 XX 06-AUG-2001 (first entry)
 XX DNA cassette for tRNAval-linked ribozyme TAR GUU Rz.
 XX Ribozyme; constitutive transport element; virucide; gene therapy;
 KW HIV-1; tRNAval; promoter; ss.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Synthetic.
 XX Key Location/Qualifiers
 FT promoter 1..91
 FT /tag= a
 FT /note= "tRNAval with 3' modification"
 FT misc_feature 92..131
 FT /tag= b
 FT /note= "TAR GUU Rz"
 FT terminator 147..151
 FT /tag= c
 XX EP1097993-A2.
 XX 09-MAY-2001.
 XX 03-NOV-2000; 2000EP-0250368.
 XX 05-NOV-1999; 99JP-0316133.
 XX (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
 XX (TAIR/) TAIRA K.
 XX Taira K, Warashina M, Kuwabara T, Kawasaki H;
 XX WPI; 2001-357832/38.
 XX Novel chimeric molecule useful for clarifying biological function of
 PT target nucleic acid and for treating viral diseases, and Alzheimer's
 PT disease, comprises region with binding affinity for molecule capable of
 PT sliding -
 PS Example 1; Page 13; 76pp; English.
 XX The present sequence is that of a DNA cassette forming part of a
 CC ribozyme expression vector of the invention. The cassette
 CC comprises the human placental tRNAval promoter (see AAF90356), with
 CC a 3' modification, and a DNA sequence corresponding to HIV-1
 CC mRNA-targeted ribozyme TAR GUU Rz (see AAF90354). Chimeric

CC molecules of the invention include ribozymes such as TAR GUU Rz
 CC linked to a constitutive transport element (see AAF90344), and
 CC expression vectors for such chimeric molecules. These are used in
 CC a claimed method to prevent or treat viral diseases, diseases
 CC associated with apoptosis or diseases associated with abnormal
 CC gene expression. They are also used in a claimed method of
 CC specifically cleaving a target nucleic acid, especially a viral
 CC gene, protooncogene or a gene associated with apoptosis. Use
 CC of the CRE facilitates cleavage of RNA previously considered
 CC refractory because of local structure.
 XX Sequence 151 BP; 38 A; 39 C; 38 G; 36 T; 0 other;
 SQ Query Match 62.7%; Score 84.6; DB 22; Length 151;
 Best Local Similarity 69.7%; Pred. No. 1.3e-19;
 Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ACGUGUGUUCGUGAGUGGUGUACGUGUCCUACACGCGAAGGUGCCCGG 60
 Db 1 ACGUGUGUUCGUGAGUGGUGUACGUGUCCUACACGCGAAGGUGCCCGG 60
 QY 61 UUCGAAACCGGCGACUACACACACACGAGGAC 99
 Db 61 TTCGAAACCGGCGACUACACACACACGAGGAC 99
 RESULT 9
 AAF90358
 ID AAF90358 standard; DNA; 320 BP.
 XX AAF90358;
 XX 06-AUG-2001 (first entry)
 XX tRNAval-linked ribozyme TAR GUU Rz-CTE.
 XX Ribozyme; constitutive transport element; virucide; gene therapy;
 KW HIV-1; tRNAval; promoter; ss.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Synthetic.
 OS Chimeric - Simian mason-pfizer type d retrovirus.
 XX Key Location/Qualifiers
 FT promoter 1..91
 FT /tag= a
 FT /note= "tRNAval with 3' modification"
 FT misc_feature 92..131
 FT /tag= b
 FT /note= "TAR GUU Rz"
 FT misc_feature 138..309
 FT /tag= c
 FT /note= "constitutive transport element"
 FT terminator 316..320
 FT /tag= d
 XX EP1097993-A2.
 XX 09-MAY-2001.
 XX 03-NOV-2000; 2000EP-0250368.
 XX 05-NOV-1999; 99JP-0316133.
 XX (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
 XX (TAIR/) TAIRA K.
 XX Taira K, Warashina M, Kuwabara T, Kawasaki H;
 XX WPI; 2001-357832/38.
 XX Novel chimeric molecule useful for clarifying biological function of
 PT target nucleic acid and for treating viral diseases, and Alzheimer's


```

XX ABZ21216;
XX AC
XX DT
XX DE
XX DE Nucleotide sequence of ribozyme expressing cassette, SEQ ID 5.
XX KW Antiviral; gene therapy; ribozyme expression cassette;
XX KW tetracyclin operator; promoter; ribozyme; anti-HIV; ds.
XX OS Synthetic.
XX DN JP2002262880-A.
XX PD 17-SEP-2002.
XX PF 09-MAR-2001; 2001JP-0067253.
XX PR 09-MAR-2001; 2001JP-0067253.
XX PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX PA (TAKE/) TAKEBE Y.
XX PA (OKAW/) OKAWA J.
XX DR WPI; 2003-132124/13.
XX PT Ribozyme expression cassette, useful for preparing a cell insensitive
XX PT to HIV and for inhibiting growth of HIV, comprises a tetracyclin
XX PT operator, at least one promoter and a sequence encoding a ribozyme
XX PT successively from the upstream side -
XX PS Disclosure; Page 16; 27pp; Japanese.
XX CC The present invention relates to a ribozyme expression cassette
XX CC comprising a tetracyclin operator, at least one promoter and a DNA
XX CC sequence encoding a ribozyme successively from the 5' end. The
XX CC tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from
XX CC the transcription initiating site of the promoter. The expression
XX CC cassette is useful in a method for preparing a cell having no sensitivity
XX CC to HIV, and for inhibiting the growth of HIV. The present invention was
XX CC used to illustrate the invention.
XX SQ Sequence 175 BP; 47 A; 39 C; 41 G; 48 T; 0 other;
Query Match 66.2%; Score 89.4; DB 25; Length 175;
Best Local Similarity 64.1%; Pred. No. 2.9e-21;
Matches 93; Conservative 26; Mismatches 16; Indels 10; Gaps 1;
Qy 1 ACCGUUGUUCGUGAGUGUGUUAUCACGUUCGCCUACACGCGAAAGUCCCGG 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 29 ACCGTTGGTTCCGTAGTGTAGTGTATCAGCTTGCCTTAACACGCGAAAGTCCCGG 88
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 UUGAAACCGCGGACUACAAAC-----AACUGAGAGACCGAAAGUCCG 110
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 89 TTCGAAACCGCGGACACTACAAACACCAACGATTGCTGCTGAGGAGCGAAAGTCCG 148
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 111 AAACGGCGACGUGCGGAAACGGUUU 135
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 149 AAACACTGTATTCCGGAACGGTTT 173
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
RESULT 5
AAAF90396
ID AAF90396 standard; RNA; 142 BP.
XX AC AAF90396;
XX DT 06-AUG-2001 (first entry)
XX DE Mouse procaspase-3 mRNA targeted ribozyme CPP Rz5.
XX KW Ribozyme; constitutive transport element; mouse; procaspase-3;
XX KW CPP32; apoptosis; gene therapy; ss.

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```

XX OS Synthetic.
XX PN EPI097993-A2.
XX PD 09-MAY-2001.
XX PF 03-NOV-2000; 2000EP-0250368.
XX PR 05-NOV-1999; 99JP-0316133.
XX PA (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
XX PA (TAIR/) TAIRA K.
XX PI Taira K, Warashina M, Kuwabara T, Kawasaki H;
XX DR WPI; 2001-357832/38.
XX PT Novel chimeric molecule useful for clarifying biological function of
XX PT target nucleic acid and for treating viral diseases, and Alzheimer's
XX PT disease, comprises region with binding affinity for molecule capable of
XX PT sliding -
XX PS Example 1; Page 49; 76pp; English.
XX CC The present sequence is that of novel ribozyme CPP Rz5, which is
XX CC targeted to a stem-structured site in mouse CPP32 mRNA that was
XX CC previously considered inaccessible. CPP32 is an apoptosis-related
XX CC gene encoding procaspase-3. CPP Rz5 was used to demonstrate the high
XX CC efficacy of hybrid ribozymes linked to a constitutive transport
XX CC element (CTE, See AAF30944) for inhibition gene expression.
XX CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see
XX CC AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme
XX CC expression plasmids and procaspase-3 expression levels were
XX CC determined by Western blotting after 36 hr. CTE-linked ribozymes
XX CC were more effective than their conventional counterparts for
XX CC inhibiting CPP32 gene expression. The CTE moiety facilitates
XX CC cleavage of RNA previously considered refractory because of local
XX CC high-order structure. It binds to RNA helicase A, which has
XX CC functions of binding to RNA, sliding and unwinding its high-order
XX CC structure. Chimeric molecules of the invention, including
XX CC CTE-ribozymes, and expression vectors, are used to prevent or
XX CC treat viral diseases, diseases associated with apoptosis or
XX CC diseases associated with abnormal gene expression (claimed). They
XX CC are also used in a claimed method of specifically cleaving a target
XX CC nucleic acid, especially a viral gene, protooncogene or a gene
XX CC associated with apoptosis.
XX SQ Sequence 142 BP; 39 A; 37 C; 37 G; 29 U; 0 other;
Query Match 64.7%; Score 87.4; DB 22; Length 142;
Best Local Similarity 79.8%; Pred. No. 1.3e-20;
Matches 103; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 1 ACCGUUGGUUCCGUGAGUGUGUUAUCACGUUCGCCUACACGCGAAAGUCCCGG 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 ACCGUUGGUUCCGUGAGUGUGUUAUCACGUUCGCCUACACGCGAAAGUCCCGG 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 UUCGAAACCGGGCACUACAAACACACACUGAGAGACCGAAGUCCGAAACGGGCAC 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 UUCGAAACCGGGCACUACAAACACCAACACUUCUAGAGAGCGGAGUCUAGAGGCCGAAA 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 121 GUCCGAAAC 129
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 GUCCGAAAC 129
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
RESULT 6
AAZ58601/c
ID AAZ58601 standard; DNA; 109 BP.
XX AC AAZ58601;
XX XX

```

CC The invention provides nucleotide sequences of hammerhead ribozymes that can be used as antiviral and gene expression suppression agents.
 CC The ribozymes have high stability in vivo. The present sequence represents an example of such a ribozyme.

SQ Sequence 136 BP; 36 A; 35 C; 37 G; 28 U; 0 other;

Query Match 100.0%; Score 135; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUAUACAGUUCGCCUAACACGCGAAAGGUCGCCGG 60

DB 1 ACCGUGGUGUCCGAGUGAGUGGUAUACAGUUCGCCUAACACGCGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGGACACUACAACACACACUAGAGGAGCCGAAAGGUCGAAACGGGCAC 120

DB 61 UUCGAAACCGGGACACUACAACACACUAGAGGAGCCGAAAGGUCGAAACGGGCAC 120

QY 121 GUCGGAACGGGUUU 135

DB 121 GUCGGAACGGGUUU 135

RESULT 2

AAZ58591
 ID AAZ58591 standard; RNA; 142 BP.

XX AC AAZ58591;

XX DT 31-MAR-2000 (first entry)

XX DE Nucleotide sequence of hammerhead ribozyme Rz3.

XX KW Hammerhead ribozyme; antiviral; gene expression; ss.

XX OS Synthetic.

XX PN JP2990268-B1.

XX PD 13-DEC-1999.

XX PF 31-AUG-1998; 98JP-0244755.

XX PR 31-AUG-1998; 98JP-0244755.

XX PA (AGEN) KOGYO GIJUTSUINCHO.

XX DR WPI; 2000-075225/07.

XX PT Nucleotide sequence of ribozyme useful as antiviral and gene expression suppression agents -

XX PS Claim 1; Page 1; 24pp; Japanese.

XX CC The invention provides nucleotide sequences of hammerhead ribozymes that can be used as antiviral and gene expression suppression agents.

XX CC The ribozymes have high stability in vivo. The present sequence represents an example of such a ribozyme.

SQ Sequence 142 BP; 39 A; 38 C; 37 G; 28 U; 0 other;

Query Match 88.1%; Score 119; DB 21; Length 142;
 Best Local Similarity 95.7%; Pred. No. 1.4e-31;
 Matches 135; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUAUACAGUUCGCCUAACACGCGAAAGGUCGCCGG 60

DB 1 ACCGUGGUGUCCGAGUGAGUGGUAUACAGUUCGCCUAACACGCGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGGACACUACAACACCAACACACUAGAGGAGCCGAAAGGUCGGAAC 114

DB 61 UUCGAAACCGGGACACUACAACACCAACACACUAGAGGAGCCGAAAGGUCGGAAC 120

QY 115 GGGCAGCUGCGAAACGGUUUU 135
 DB 121 GGGCAGCUGCGAAACGGUUUU 141

RESULT 3

ABZ21217
 ID ABZ21217 standard; DNA; 175 BP.

XX AC ABZ21217;

XX DT 04-APR-2003 (first entry)

XX DE Nucleotide sequence of ribozyme expressing cassette, SEQ ID 6.

XX KW Antiviral; gene therapy; ribozyme expression cassette; tetracyclin operator; promoter; ribozyme; anti-HIV; ds.

XX OS Synthetic.

XX PN JP2002262880-A.

XX PD 17-SEP-2002.

XX PF 09-MAR-2001; 2001JP-0067253.

XX PR 09-MAR-2001; 2001JP-0067253.

XX PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.

XX PA (TAKE/) TAKEBE Y.

XX PA (OKAW/) OKAWA J.

XX DR WPI; 2003-132124/13.

XX PT Ribozyme expression cassette, useful for preparing a cell insensitive to HIV and for inhibiting growth of HIV, comprises a tetracyclin operator, at least one promoter and a sequence encoding a ribozyme successively from the upstream side -

XX PS Disclosure; Page 16; 27pp; Japanese.

XX CC The present invention relates to a ribozyme expression cassette comprising a tetracyclin operator, at least one promoter and a DNA sequence encoding a ribozyme successively from the 5' end. The tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from the transcription initiating site of the promoter. The expression cassette is useful in a method for preparing a cell having no sensitivity to HIV, and for inhibiting the growth of HIV. The present sequence was used to illustrate the invention.

XX SQ Sequence 175 BP; 48 A; 40 C; 41 G; 46 T; 0 other;

Query Match 67.6%; Score 91.2; DB 25; Length 175;
 Best Local Similarity 69.2%; Pred. No. 6.8e-22;
 Matches 101; Conservative 26; Mismatches 8; Indels 11; Gaps 2;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUAUACAGUUCGCCUAACACGCGAAAGGUCGCCGG 60

DB 29 ACCGTGTGTTCCGTAGTAGTGTGTTATCATCGCTACACGCGAAAGGTCGCCGG 88

QY 61 UUCGAAACCGGGACACUACAACAC-----AACACUGAGAGGACCGAAAGGUCGG 110

DB 89 TTCGAAACCGGGACACTACAAAAACCAACGATAGATGCTGATGAGGACCGAAAGTCGG 148

QY 111 AAAC-GGGCAGCUGCGAAACGGUUUU 135

DB 149 AAATTGACACTCCGGAACGGTTTT 174

RESULT 4

ABZ21216

ID ABZ21216 standard; DNA; 175 BP.

GenCore version 5.1.16
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 08:06:21 ; Search time 195.652 Seconds
(without alignments)
1862.612 Million cell updates/sec

Title: US-09-763-590-1

Perfect score: 135

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	100.0	136	21	AAZ58590 Nucleotide sequenc
2	119	88.1	142	21	AAZ58591 Nucleotide sequenc
3	91.2	67.6	175	25	ABZ21217 Nucleotide sequenc
4	89.4	66.2	175	25	ABZ21216 Nucleotide sequenc
5	87.4	64.7	142	22	AAF90396 Mouse procaspase-3
6	85.4	63.3	109	21	AAZ58601 Sequence of a lowe
7	85.4	63.3	137	24	ABK51149 tRNA-Luc GUA Rz Ri
8	84.6	62.7	151	22	AAF90357 DNA cassette for t

9	84.6	62.7	320	22	AAF90358 tRNAVal-linked rib
10	82.8	61.3	88	20	AAZ10600 Nucleotide sequenc
11	82.8	61.3	88	24	AAZ40450 Nucleotide related t
12	82.8	61.3	88	25	ABX12785 Human RNA sequence
13	82.8	61.3	100	22	AAH47825 Human tRNA promote
14	82.8	61.3	117	25	ABZ21212 tet O1-tRNAVal seq
15	82.8	61.3	138	24	AAZ40467 Maxizyme related t
16	82.8	61.3	141	22	AAF90395 Mouse procaspase-3
17	82.8	61.3	142	22	AAF90392 Mouse procaspase-3
18	82.8	61.3	142	22	AAF90393 Mouse procaspase-3
19	82.8	61.3	142	22	AAF90394 Mouse procaspase-3
20	78	57.8	128	21	AAZ58592 Nucleotide sequenc
c 21	74.2	55.0	325	17	AAI09849 Plasmid pBTv1-434
c 22	74.2	55.0	332	17	AAI09852 Plasmid pBTv1-434
c 23	74.2	55.0	406	17	AAI09850 Plasmid pZIP VI-43
c 24	74.2	55.0	406	17	AAI09851 Plasmid pZIP VI-43
c 25	73.4	54.4	149	21	AAZ58594 Nucleotide sequenc
26	73	54.1	95	21	AAZ58593 Nucleotide sequenc
27	73	54.1	95	22	AAF90356 Human placental tr
28	73	54.1	269	17	AAI09848 Plasmid pBTv1. Syn
c 29	73	54.1	139904	24	AAZ83562 Human cDNA differe
30	69.8	51.7	132	18	AAI92275 Pol III transcript
31	69.8	51.7	132	19	AAV57890 pol III transcript
32	69.8	51.7	132	22	AAZ60208 Cassette pMTJ. Sy
c 33	66.8	49.5	113	21	AAZ58596 Sequence of an ant
34	66	48.9	110	21	AAZ58595 Sequence of a sens
c 35	63.8	47.3	43226	20	AAZ60263 Nucleic acid sequ
36	54.4	40.3	2451	23	ABL24834 Drosophila melanog
37	53.6	39.7	4689	23	ABL02136 Drosophila melanog
38	53.4	39.6	2289	23	ABL04712 Drosophila melanog
c 39	53.2	39.4	3886	23	ABL24836 Drosophila melanog
c 40	53.2	39.4	22967	23	ABL12942 Drosophila melanog
41	50	37.0	7799	23	ABL30068 Drosophila melanog
c 42	50	37.0	7799	23	ABL30068 Drosophila melanog
c 43	50	37.0	27433	23	ABL20312 Drosophila melanog
c 44	47	34.8	106	21	AAZ58602 Sequence of a lowe
c 45	45	33.3	4034	23	ABL16732 Drosophila melanog

ALIGNMENTS

RESULT 1

AAZ58590
ID AAZ58590 standard; RNA; 136 BP.
XX
AC AAZ58590;
XX
DT 31-MAR-2000 (first entry)
XX
DE Nucleotide sequence of hammerhead ribozyme Rz2.
XX
KW Hammerhead ribozyme; antiviral; gene expression; ss.
XX
OS Synthetic.
XX
PN JP2990268-B1.
XX
PD 13-DEC-1999.
XX
PF 31-AUG-1998; 98JP-0244755.
XX
PR 31-AUG-1998; 98JP-0244755.
XX
PA (AGEN) KOGYO GIJUTSUINCHO.
XX
DR WPI; 2000-075225/07.
XX
PT Nucleotide sequence of ribozyme useful as antiviral and gene expression
suppression agents -
XX
XX Claim 1; Page 1; 24pp; Japanese.
XX

KW CPP32; apoptosis; gene therapy; ss.
 XX Synthetic.
 OS
 XX
 PN EPI097993-A2.
 XX
 PD 09-MAY-2001.
 XX
 PF 03-NOV-2000; 2000EP-0250368.
 XX
 PR 05-NOV-1999; 99JP-0316133.
 XX
 PA (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
 XX
 PI (TAIR/) TAIRA K.
 XX
 PI Taira K, Warashina M, Kuwabara T, Kawasaki H;
 XX
 DR WPI; 2001-357832/38.
 XX
 XX Novel chimeric molecule useful for clarifying biological function of
 PT target nucleic acid and for treating viral diseases, and Alzheimer's
 PT disease, comprises region with binding affinity for molecule capable of
 PT sliding
 XX
 PS Example 1; Page 47; 76pp; English.
 XX
 CC The present sequence is that of novel ribozyme CPP Rz2, which is
 CC targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related
 CC gene encoding procaspase-3. CPP Rz2 was used to demonstrate the high
 CC efficacy of hybrid ribozymes linked to a constitutive transport
 CC element (CTE, See AAF30944) for inhibition gene expression.
 CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see
 CC AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme
 CC expression plasmids and procaspase-3 expression levels were
 CC determined by Western blotting after 36 hr. CTE-linked ribozymes
 CC were more effective than their conventional counterparts for
 CC inhibiting CPP32 gene expression. The CTE moiety facilitates
 CC cleavage of RNA previously considered refractory because of local
 CC high-order structure. It binds to RNA helicase A, which has
 CC functions of binding to RNA, sliding and unwinding its high-order
 CC structure. Chimeric molecules of the invention, including
 CC CTE-ribozymes, and expression vectors, are used to prevent or
 CC treat viral diseases, diseases associated with apoptosis or
 CC diseases associated with abnormal gene expression (claimed). They
 CC are also used in a claimed method of specifically cleaving a target
 CC nucleic acid, especially a viral gene, protooncogene or a gene
 CC associated with apoptosis.
 XX
 SQ Sequence 142 BP; 38 A; 36 C; 35 G; 33 U; 0 other;
 Query Match 57.4%; Score 81; DB 22; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGUGGUGUCCGUGAGUGGUAUCACGUCGCUAACACGCGAAAGGUCCCGG 60
 DB 1 ACCGUGGUGUCCGUGAGUGGUAUCACGUCGCUAACACGCGAAAGGUCCCGG 60
 QY 61 UUCGAAACCGGGCACUACAAA 81
 DB 61 UUCGAAACCGGGCACUACAAA 81
 RESULT 15
 AAF90394
 ID AAF90394 standard; RNA; 142 BP.
 XX
 AC AAF90394;
 XX
 XX 06-AUG-2001 (first entry)
 XX
 DE Mouse procaspase-3 mRNA targeted ribozyme CPP Rz3.
 XX

KW Ribozyme; constitutive transport element; mouse; procaspase-3;
 KW CPP32; apoptosis; gene therapy; ss.
 XX Synthetic.
 OS
 XX
 PN EPI097993-A2.
 XX
 PD 09-MAY-2001.
 XX
 PF 03-NOV-2000; 2000EP-0250368.
 XX
 PR 05-NOV-1999; 99JP-0316133.
 XX
 PA (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
 XX
 PI (TAIR/) TAIRA K.
 XX
 PI Taira K, Warashina M, Kuwabara T, Kawasaki H;
 XX
 DR WPI; 2001-357832/38.
 XX
 XX Novel chimeric molecule useful for clarifying biological function of
 PT target nucleic acid and for treating viral diseases, and Alzheimer's
 PT disease, comprises region with binding affinity for molecule capable of
 PT sliding
 XX
 PS Example 1; Page 48; 76pp; English.
 XX
 CC The present sequence is that of novel ribozyme CPP Rz3, which is
 CC targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related
 CC gene encoding procaspase-3. CPP Rz3 was used to demonstrate the high
 CC efficacy of hybrid ribozymes linked to a constitutive transport
 CC element (CTE, See AAF30944) for inhibition gene expression.
 CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see
 CC AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme
 CC expression plasmids and procaspase-3 expression levels were
 CC determined by Western blotting after 36 hr. CTE-linked ribozymes
 CC were more effective than their conventional counterparts for
 CC inhibiting CPP32 gene expression. The CTE moiety facilitates
 CC cleavage of RNA previously considered refractory because of local
 CC high-order structure. It binds to RNA helicase A, which has
 CC functions of binding to RNA, sliding and unwinding its high-order
 CC structure. Chimeric molecules of the invention, including
 CC CTE-ribozymes, and expression vectors, are used to prevent or
 CC treat viral diseases, diseases associated with apoptosis or
 CC diseases associated with abnormal gene expression (claimed). They
 CC are also used in a claimed method of specifically cleaving a target
 CC nucleic acid, especially a viral gene, protooncogene or a gene
 CC associated with apoptosis.
 XX
 SQ Sequence 142 BP; 37 A; 40 C; 34 G; 31 U; 0 other;
 Query Match 57.4%; Score 81; DB 22; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGUGGUGUCCGUGAGUGGUAUCACGUCGCUAACACGCGAAAGGUCCCGG 60
 DB 1 ACCGUGGUGUCCGUGAGUGGUAUCACGUCGCUAACACGCGAAAGGUCCCGG 60
 QY 61 UUCGAAACCGGGCACUACAAA 81
 DB 61 UUCGAAACCGGGCACUACAAA 81
 Search completed: September 13, 2003, 09:52:33
 Job time : 205.848 secs

```

FT      stem_loop      /*tag= d
FT      56..72
FT      /*tag= e
FT      misc_binding
FT      73..78
FT      /*tag= f
FT      /bound_moiety= "trna-val_T-MzL"
FT      /note= "Forms a double-stranded region with nucleotides
FT      19-14 of itself"
FT      81..88
FT      /*tag= g
FT      /bound_moiety= "trna-val_T-MzL"
FT      /note= "Forms a double-stranded region with nucleotides
FT      11-4 of itself"
FT      95..107
FT      /*tag= h
FT      stem_loop
FT      111..128
FT      /*tag= i
FT
XX      JP2002119283-A.
XX
XX      23-APR-2002.
XX
XX      13-OCT-2000; 2000JP-0313320.
XX
XX      13-OCT-2000; 2000JP-0313320.
XX
XX      (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
XX
XX      WPI; 2002-483792/52.
XX
XX      A nucleic acid enzyme which has selective and effective eradicating
XX      activity towards harmful cells by acquiring cleavage activity of a
XX      specific target RNA by recognition of the other RNA molecule
XX
XX      Disclosure; Fig 7; 17pp; Japanese.
XX
XX      The invention relates to a nucleic acid enzyme with modifiable RNA
XX      cleavage activity. More specifically the invention relates to a nucleic
XX      acid enzyme, trans maxizyme, which has selective and effective
XX      eradicating activity towards harmful cells by acquiring cleavage activity
XX      of a specific target RNA by recognition of the other RNA molecule. The
XX      enzyme of the invention is useful for cleaving target RNA and is useful
XX      in treating diseases caused by the target RNA. This polynucleotide
XX      sequence represents the trna-val T-MzL sequence related to the maxizyme
XX      enzyme of the invention.
XX
XX      Sequence 138 BP; 31 A; 38 C; 32 G; 37 U; 0 other;
XX
XX      Query Match      57.4%; Score 81; DB 24; Length 138;
XX      Best Local Similarity 100.0%; Pred. No. 2.1e-18;
XX      Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUAACACGCGAAAGUCCCGG 60
XX      |
XX      Db      1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUAACACGCGAAAGUCCCGG 60
XX      |
XX      QY      61 UUCGAAACCGGGCACUACAAA 81
XX      |
XX      Db      61 UUCGAAACCGGGCACUACAAA 81
XX      |
XX
XX      RESULT 13
XX      ID      AAF90392
XX      AC      AAF90392;
XX      DT      06-AUG-2001 (first entry)
XX      DE      Mouse procaspase-3 mRNA targeted ribozyme CPP Rz1.
XX      KW      Ribozyme; constitutive transport element; mouse; procaspase-3;
XX      CPP32; apoptosis; gene therapy; ss.

```

```

XX      Synthetic.
XX      EPI097993-A2.
XX
XX      09-MAY-2001.
XX
XX      03-NOV-2000; 2000EP-0250368.
XX
XX      05-NOV-1999; 99JP-0316133.
XX
XX      (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
XX      (TAIR/) TAIRA K.
XX
XX      Taira K, Warashina M, Kuwabara T, Kawasaki H;
XX      WPI; 2001-357832/38.
XX
XX      Novel chimeric molecule useful for clarifying biological function of
XX      target nucleic acid and for treating viral diseases, and Alzheimer's
XX      disease, comprises region with binding affinity for molecule capable of
XX      sliding
XX
XX      Example 1; Page 47; 76pp; English.
XX
XX      The present sequence is that of novel ribozyme CPP Rz1, which is
XX      targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related
XX      gene encoding procaspase-3. CPP Rz1 was used to demonstrate the high
XX      efficacy of hybrid ribozymes linked to a constitutive transport
XX      element (CTE, See AAF30944) for inhibition gene expression.
XX      5 Ribozymes for different sites in CPP32 mRNA were designed (see
XX      AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme
XX      expression plasmids and procaspase-3 expression levels were
XX      determined by Western blotting after 36 hr. CTE-linked ribozymes
XX      were more effective than their conventional counterparts for
XX      inhibiting CPP32 gene expression. The CTE moiety facilitates
XX      cleavage of RNA previously considered refractory because of local
XX      high-order structure. It binds to RNA helicase A, which has
XX      functions of binding to RNA, sliding and unwinding its high-order
XX      structure. Chimeric molecules of the invention, including
XX      CTE-ribozymes, and expression vectors, are used to prevent or
XX      treat viral diseases, diseases associated with apoptosis or
XX      diseases associated with abnormal gene expression (claimed). They
XX      are also used in a claimed method of specifically cleaving a target
XX      nucleic acid, especially a viral gene, protooncogene or a gene
XX      associated with apoptosis.
XX
XX      Sequence 142 BP; 36 A; 42 C; 37 G; 27 U; 0 other;
XX
XX      Query Match      57.4%; Score 81; DB 22; Length 142;
XX      Best Local Similarity 100.0%; Pred. No. 2.1e-18;
XX      Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUAACACGCGAAAGUCCCGG 60
XX      |
XX      Db      1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUAACACGCGAAAGUCCCGG 60
XX      |
XX      QY      61 UUCGAAACCGGGCACUACAAA 81
XX      |
XX      Db      61 UUCGAAACCGGGCACUACAAA 81
XX      |
XX
XX      RESULT 14
XX      ID      AAF90393
XX      AC      AAF90393 standard; RNA; 142 BP.
XX      AC      AAF90393;
XX      DT      06-AUG-2001 (first entry)
XX      DE      Mouse procaspase-3 mRNA targeted ribozyme CPP Rz2.
XX      KW      Ribozyme; constitutive transport element; mouse; procaspase-3;

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[illegible]

CC sequence represents the tRNA-val promoter sequence relating to the
 CC maxizyme enzyme of the invention.

SQ Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;

Query Match 57.4%; Score 81; DB 24; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGAGUGAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGG 60
 |||||
 Db 1 ACCGUGGUUCCGAGUGAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGGCACUACAAA 81
 |||||

Db 61 UUCGAAACCGGGCACUACAAA 81

RESULT 9

ABX12785

ID ABX12785 standard; RNA; 88 BP.

XX ABX12785;

DT 15-MAY-2003 (first entry)

XX Human RNA sequence relating to novel maxizyme.

XX Human; maxizyme; target mRNA; helicase activity; viral disease;
 KW human immunodeficiency virus; HIV; hepatitis C; cancer;
 KW apoptosis-associated disease; Alzheimer's disease; Parkinson's disease;
 KW autoimmune disease; inflammatory disease; genetic disorder;
 KW mRNA cleavage; virucide; neurotropic; antiparkinsonian; cytostatic;
 KW antiinflammatory; immunosuppressive; ss.

XX Homo sapiens.

XX WO200292821-A1.

PN 21-NOV-2002.

PD 30-APR-2002; 2002WO-JP04322.

PF 01-MAY-2001; 2001JP-0134469.

PR (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (TAIS) TAISHO PHARM CO LTD.

PA (GENO-) GENOFUNCTION INC.

PI Taira K, Warashina T, Warashina M, Kawasaki H, Hara T, Norawa I;

XX WPI; 2003-129298/12.

DR Maxizyme binding to a molecule with helicase activity for treatment of

PT viral infection cancer and autoimmune disease

PS Claim 11; Page 30-31; 36pp; Japanese.

XX The present invention relates to a novel maxizyme that can bind to a
 CC target mRNA molecule or a molecule having helicase activity. The
 CC maxizyme is useful for the prevention and treatment of viral diseases
 CC such as human immunodeficiency virus (HIV), hepatitis C or hepatitis B,
 CC apoptosis-associated diseases such as Alzheimer's and Parkinson's
 CC diseases, cancer, autoimmune diseases, inflammatory diseases and
 CC genetic disorders. The maxizyme binds to and cleaves target mRNA
 CC irrespective of the higher-order structure of the latter. The present
 CC sequence represents a human RNA sequence relating to the present
 CC invention.

XX Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;

Query Match 57.4%; Score 81; DB 25; Length 88;

Best Local Similarity 100.0%; Pred. No. 1.9e-18;

Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGAGUGAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGG 60
 |||||

Db 1 ACCGUGGUUCCGAGUGAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGGCACUACAAA 81
 |||||

Db 61 UUCGAAACCGGGCACUACAAA 81

RESULT 10

ABZ21212

ID ABZ21212 standard; DNA; 117 BP.

XX ABZ21212;

XX 04-APR-2003 (first entry)

DT tet 01-tRNAval sequence, SEQ ID 1.

XX Antiviral; gene therapy; ribozyme expression cassette;

XX tetracyclin operator; promoter; ribozyme; anti-HIV; ds.

XX Synthetic.

XX OS JP2002262880-A.

PN 17-SEP-2002.

PD 09-MAR-2001; 2001JP-0067253.

PF 09-MAR-2001; 2001JP-0067253.

PR (KOKU-) KOKURITSU YOSO EISEI KENKYUSHO.

XX (TAKE/) TAKEBE Y.

XX (OKAW/) OKAWA J.

XX WPI; 2003-132124/13.

XX Ribozyme expression cassette, useful for preparing a cell insensitive

XX to HIV and for inhibiting growth of HIV, comprises a tetracyclin

XX operator, at least one promoter and a sequence encoding a ribozyme

XX successively from the upstream side

XX Claim 6; Page 15; 27pp; Japanese.

XX The present invention relates to a ribozyme expression cassette

XX comprising a tetracyclin operator, at least one promoter and a DNA

XX sequence encoding a ribozyme successively from the 5' end. The

XX tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from

XX the transcription initiating site of the promoter. The expression

XX cassette is useful in a method for preparing a cell having no sensitivity

XX to HIV, and for inhibiting the growth of HIV. To illustrate the

XX invention, a tet 01-human tRNAval promoter cassette was constructed,

XX using the present sequence.

XX Sequence 117 BP; 31 A; 28 C; 26 G; 32 T; 0 other;

Query Match 57.4%; Score 81; DB 25; Length 117;

Best Local Similarity 76.5%; Pred. No. 2e-18;

Matches 62; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGAGUGAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGG 60
 |||||

Db 29 ACCGTTGGTTCCGTTAGTGTATACGTTTCGCTTAACACGCGAAAGGTCGCCGG 88

QY 61 UUCGAAACCGGGCACUACAAA 81
 :|||||

Db 89 TTCGAAACCGGGCACUACAAA 109

RESULT 11

PT disease, comprises region with binding affinity for molecule capable of
 PT sliding -
 XX
 PS Example 1; Page 48; 76pp; English.
 XX
 CC The present sequence is that of novel ribozyme CPP R23, which is
 CC targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related
 CC gene encoding procaspase-3. CPP R23 was used to demonstrate the high
 CC efficacy of hybrid ribozymes linked to a constitutive transport
 CC element (CTE). See AAF30944 for inhibition gene expression.
 CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see
 CC AA90392-96). Mouse NIH3T3 cells were transfected with ribozyme
 CC expression plasmids and procaspase-3 expression levels were
 CC determined by Western blotting after 36 hr. CTE-linked ribozymes
 CC were more effective than their conventional counterparts for
 CC inhibiting CPP32 gene expression. The CTE moiety facilitates
 CC cleavage of RNA previously considered refractory because of local
 CC high-order structure. It binds to RNA helicase A, which has
 CC functions of binding to RNA, sliding and unwinding its high-order
 CC structure. Chimeric molecules of the invention, including
 CC CTE-ribozymes, and expression vectors, are used to prevent or
 CC treat viral diseases, diseases associated with apoptosis or
 CC diseases associated with abnormal gene expression (claimed). They
 CC are also used in a claimed method of specifically cleaving a target
 CC nucleic acid, especially a viral gene, protooncogene or a gene
 CC associated with apoptosis.
 XX
 SQ Sequence 141 BP; 37 A; 37 C; 35 G; 32 U; 0 other;
 Query Match 58.6%; Score 82.6; DB 22; Length 141;
 Best Local Similarity 80.2%; Pred. No. 5.9e-19;
 Matches 97; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 ACCGUGGUUCCGUGAGUGUGUUAUCACGAGGACGCGGAAAGGUCGCCG 60
 Db 1 ACCGUGGUUCCGUGAGUGUGUUAUCACGAGGACGCGGAAAGGUCGCCG 60
 QY 61 UUCGAAACCGGGCACACACACACACACACACACACACACACACACAC 120
 Db 61 UUCGAAACCGGGCACACACACACACACACACACACACACACACACAC 120
 QY 121 G 121
 Db 121 G 121
 RESULT 7
 AA210600
 ID AA210600 standard; RNA; 88 BP.
 AC AA210600;
 XX
 DT 17-NOV-1999 (first entry)
 XX
 DE Nucleotide sequence of tRNA-val.
 XX
 KW Nucleic acid enzyme; maxizyme; allosteric RNA-cleaving activity;
 KW RNA cleavage; chronic myeloid leukemia;
 KW Philadelphia chromosome abnormality; ss.
 XX
 OS Synthetic.
 XX
 PN WO9946388-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99WO-JP01187.
 XX
 PR 12-MAR-1998; 98JP-0060969.
 PR 30-OCT-1998; 98JP-0311098.
 XX
 XX (TAIS) TAISHO PHARM CO LTD.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

XX
 PI Taira K, Kuwabara T, Hitoshio A;
 XX
 DR WPI; 1999-551415/46.
 XX
 PT Nucleic acid enzyme having allosteric RNA-cleaving activity, used for
 PT treatment of chronic myeloid leukemia -
 XX
 PS Claim 8; Page 55; 93pp; Japanese.
 XX
 CC The specification describes nucleotide sequences which make up the
 CC left and right arms of a nucleic acid enzyme (maxizyme). The maxizyme
 CC has allosteric RNA-cleaving activity on a specific target RNA. The
 CC maxizyme can be used for efficient cleavage of RNA molecules at
 CC specific points, especially for the prevention and treatment of
 CC chronic myeloid leukemia and Philadelphia chromosome abnormality.
 CC The present sequence is used in the course of the invention.
 XX
 SQ Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;
 Query Match 57.4%; Score 81; DB 20; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGUGGUUCCGUGAGUGUGUUAUCACGAGGACGCGGAAAGGUCGCCG 60
 Db 1 ACCGUGGUUCCGUGAGUGUGUUAUCACGAGGACGCGGAAAGGUCGCCG 60
 QY 61 UUCGAAACCGGGCACACACACACACACACACACACACACACACACAC 81
 Db 61 UUCGAAACCGGGCACACACACACACACACACACACACACACACACAC 81
 RESULT 8
 AAL40450
 ID AAL40450 standard; tRNA; 88 BP.
 XX
 AC AAL40450;
 XX
 DT 19-SEP-2002 (first entry)
 XX
 DE Maxizyme related tRNA-val promoter sequence.
 XX
 KW Enzyme; modifiable RNA cleavage activity; maxizyme-constituting RNA;
 KW trans maxizyme; tRNA-val; ss.
 XX
 OS Unidentified.
 XX
 PN JP2002119283-A.
 XX
 PD 23-APR-2002.
 XX
 PF 13-OCT-2000; 2000JP-0313320.
 XX
 PR 13-OCT-2000; 2000JP-0313320.
 XX
 PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
 XX
 DR WPI; 2002-483792/52.
 XX
 PT A nucleic acid enzyme which has selective and effective eradicating
 PT activity towards harmful cells by acquiring cleavage activity of a
 PT specific target RNA by recognition of the other RNA molecule -
 XX
 PS Claim 12; Page 2; 17pp; Japanese.
 XX
 CC The invention relates to a nucleic acid enzyme with modifiable RNA
 CC cleavage activity. More specifically the invention relates to a nucleic
 CC acid enzyme, trans maxizyme, which has selective and effective
 CC eradicating activity towards harmful cells by acquiring cleavage activity
 CC of a specific target RNA by recognition of the other RNA molecule. The
 CC enzyme of the invention is useful for cleaving target RNA and is useful
 CC in treating diseases caused by the target RNA. This polynucleotide

CC The invention provides nucleotide sequences of hammerhead ribozymes
 CC that can be used as antiviral and gene expression suppression agents.
 CC The ribozymes have high stability in vivo. The present sequence
 CC represents an example of such a ribozyme.

XX SQ Sequence 142 BP; 39 A; 38 C; 37 G; 28 U; 0 other;

Query Match 100.0%; Score 141; DB 21; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.1e-39;
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCGG 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCGG 60
 QY 61 UUCGAAACCGGGCACUACAAACACACACACACACACACACACACACACACACACAC 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 UUCGAAACCGGGCACUACAAACACACACACACACACACACACACACACACACACAC 120
 QY 121 GGGCAGUCGGAACGGUUU 141
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 GGGCAGUCGGAACGGUUU 141

RESULT 2

RAZ58590
 ID AAZ58590 standard; RNA; 136 BP.

XX AC AAZ58590;
 XX 31-MAR-2000 (first entry)
 XX DE Nucleotide sequence of hammerhead ribozyme Rz2.
 XX KW Hammerhead ribozyme; antiviral; gene expression; ss.
 XX OS Synthetic.
 XX PN JP2990268-B1.
 XX PD 13-DEC-1999.

XX 31-AUG-1998; 98JP-0244755.

XX 31-AUG-1998; 98JP-0244755.

XX (AGEN) KOGYO GIJUNSUINCHO.

XX WPI; 2000-075225/07.

XX Nucleotide sequence of ribozyme useful as antiviral and gene expression suppression agents.

XX Claim 1; Page 1; 24pp; Japanese.

XX The invention provides nucleotide sequences of hammerhead ribozymes
 CC that can be used as antiviral and gene expression suppression agents.
 CC The ribozymes have high stability in vivo. The present sequence
 CC represents an example of such a ribozyme.

XX SQ Sequence 136 BP; 36 A; 35 C; 37 G; 28 U; 0 other;

Query Match 84.4%; Score 119; DB 21; Length 136;
 Best Local Similarity 95.7%; Pred. No. 1.3e-31;
 Matches 135; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCGG 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCGG 60
 QY 61 UUCGAAACCGGGCACUACAAACACACACACACACACACACACACACACACACACAC 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 UUCGAAACCGGGCACUACAA-----ACACACACACUGAGGAGGACCGAAAGGUCGGAAC 114

QY 121 GGGCAGUCGGAACGGUUU 141
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 115 GGGCAGUCGGAACGGUUU 135

RESULT 3

ABZ21217
 ID ABZ21217 standard; DNA; 175 BP.

XX AC ABZ21217;
 XX 04-APR-2003 (first entry)
 XX DE Nucleotide sequence of ribozyme expressing cassette, SEQ ID 6.
 XX KW Antiviral; gene therapy; ribozyme expression cassette;
 XX KW tetracyclin operator; promoter; ribozyme; anti-HIV; ds.
 XX OS Synthetic.
 XX PN JP2002262880-A.
 XX PD 17-SEP-2002.

XX 09-MAR-2001; 2001JP-0067253.

XX 09-MAR-2001; 2001JP-0067253.

XX (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.

XX (TAKE/) TAKEBE Y.

XX (OKAW/) OKAWA J.

XX WPI; 2003-132124/13.

XX Ribozyme expression cassette, useful for preparing a cell insensitive
 PT to HIV and for inhibiting growth of HIV, comprises a tetracyclin
 PT operator, at least one promoter and a sequence encoding a ribozyme
 PT successively from the upstream side -

XX Disclosure; Page 16; 27pp; Japanese.

XX The present invention relates to a ribozyme expression cassette
 CC comprising a tetracyclin operator, at least one promoter and a DNA
 CC sequence encoding a ribozyme successively from the 5' end. The
 CC tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from
 CC the transcription initiating site of the promoter. The expression
 CC cassette is useful in a method for preparing a cell having no sensitivity
 CC to HIV, and for inhibiting the growth of HIV. The present sequence was
 CC used to illustrate the invention.

XX SQ Sequence 175 BP; 48 A; 40 C; 41 G; 46 T; 0 other;

Query Match 67.5%; Score 95.2; DB 25; Length 175;
 Best Local Similarity 69.9%; Pred. No. 2.6e-23;
 Matches 102; Conservative 26; Mismatches 13; Indels 5; Gaps 2;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCGG 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 29 ACCGTTGGTTCCGTTAGTCTACTGCTTACAGTTCGCTACACGCGAAGGTCGCCGG 88

QY 61 UUCGAAACCGGGCACUACAAA-----CCAACACACACUGAGAGACCGAAAGGUCG 116
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 89 TTCGAAACCGGGCACACTACAAAACCAACGATAGATTGCTGATGAGGACCGAAAGGTCG 148

QY 117 AAAC-GGGCAGUCGGAACGGUUU 141
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QY 149 AAACGTGACACTCCGGAAACGGTTTT 174

RESULT 4

ABZ21216
 ID ABZ21216 standard; DNA; 175 BP.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 08:06:21 ; Search time 204.348 Seconds
(without alignments)
1862.612 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accguuguuucguagugu.....ggcacucggaacgguuuu 141

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	141	100.0	142	21	AAZ58591 Nucleotide sequenc
2	119	84.4	136	21	AAZ58590 Nucleotide sequenc
3	95.2	67.5	175	25	ABZ21217 Nucleotide sequenc
4	91.8	65.1	175	25	ABZ21216 Nucleotide sequenc
5	83.2	59.0	100	22	AAH47825 Human tRNA promote
6	82.6	58.6	141	22	AAF90395 Mouse procaspase-3
7	81	57.4	88	20	AAZ10600 Nucleotide sequenc
8	81	57.4	88	24	AAZ10450 Maxizyme related t

9	81	57.4	88	25	ABX12785 Human RNA sequence
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18	81	57.4	320	22	AAF90358 tRNAVal-linked rib
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20	73.4	52.1	149	21	AAZ58594 Nucleotide sequenc
21	73	51.8	95	21	AAZ58593 Human placental tr
22	73	51.8	95	22	AAF90356 Plasmid ptVI. Syn
23	73	51.8	269	17	AAZ09848 Plasmid pBT1-434
24	73	51.8	325	17	AAZ09849 Plasmid pBT1-434
25	73	51.8	332	17	AAZ09852 Plasmid pZIP VI-43
26	73	51.8	406	17	AAZ09850 Plasmid pZIP VI-43
27	73	51.8	406	17	AAZ09851 Human cDNA differe
28	73	51.8	139904	24	ABK83562 Pol III transcript
29	69.8	49.5	132	18	AAZ92275 Pol III transcript
30	69.8	49.5	132	19	AAZ57890 Cassette pMT. Sy
31	69.8	49.5	132	22	AAZ60208 Sequence of a lowe
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34	66	46.8	110	21	AAZ58602 Nucleic acid seque
35	65	46.1	106	21	AAZ58603 Drosophila melanog
36	63.8	45.2	43226	20	AAZ60263 Drosophila melanog
37	53.6	38.0	4669	23	ABL02136 Drosophila melanog
38	53.2	37.7	2289	23	ABL04712 Drosophila melanog
39	53.2	37.7	2451	23	ABL24834 Drosophila melanog
40	53.2	37.7	3886	23	ABL24836 Drosophila melanog
41	53.2	37.7	22967	23	ABL12942 Drosophila melanog
42	50	35.5	7799	23	ABL30068 Drosophila melanog
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ALIGNMENTS

RESULT 1
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ID AAZ58591 standard; RNA; 142 BP.
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AC AAZ58591;
XX
DT 31-MAR-2000 (first entry)
XX
DE Nucleotide sequence of hammerhead ribozyme Rz3.
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KW Hammerhead ribozyme; antiviral; gene expression; ss.
XX
OS Synthetic.
XX
PN JP2990268-B1.
XX
PD 13-DEC-1999.
XX
PF 31-AUG-1998; 98JP-0244755.
XX
PR 31-AUG-1998; 98JP-0244755.
XX
PA (AGEN) KOGYO GIJUTSUINCHO.
XX
DR WPI; 2000-075225/07.
XX
PT Nucleotide sequence of ribozyme useful as antiviral and gene expression
XX
PS Claim 1; Page 1; 24pp; Japanese.
XX

BASE COUNT 23 a 25 c 21 g 19 t
ORIGIN

Query Match 57.4%; Score 81; DB 6; Length 88;
Best Local Similarity 76.5%; Pred. No. 8.3e-13;
Matches 62; Conservative 19; Mismatches 0; Indels 0; Gaps 0;
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Search completed: September 13, 2003, 10:39:39
Job time : 1436.54 secs

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Best Local Similarity 75.3%; Pred. No. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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RESULT 13
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LOCUS      153 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
anti-mSryRNA/Rz6.
ACCESSION AB080624
VERSION AB080624.1 GI:22531657
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
Nishino,K., Nakayama,A. and Taira,K.
TITLE Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 153)
AUTHORS Tachi,C.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
Veterinary Medicine, Lab. Developmental and Reproductive
Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
LOCATION/Qualifiers
FEATURES
source
misc_rna
misc_feature
misc_feature
BASE COUNT      36 a      39 c      40 g      38 t
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Query Match      58.0%; Score 81.8; DB 12; Length 153;
Best Local Similarity 75.3%; Pred. No. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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Db 61 TTCGAACCGGGCACTACAAACCA 85
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RESULT 14
AX453846
LOCUS      88 bp      mRNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 5 from Patent EP1213351.

ACCESSION AX453846
VERSION AX453846.1 GI:21713515
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Taira,K., Warashina,M. and Warashina,T.
TITLE Nucleic acid enzymes acquiring an activity for cleaving a target
rna by recognising another molecule
JOURNAL Patent: EP 1213351-A 5 12-JUN-2002;
National Institute of Advanced Industrial Science and Technology
(JP)
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source
Location/Qualifiers
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/note="tRNAval promoter sequence"
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Best Local Similarity 76.5%; Pred. No. 8.3e-13;
Matches 62; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
BD143502
LOCUS      88 bp      RNA      linear      PAT 17-JAN-2003
DEFINITION Nucleic acid enzyme acquiring activity of cleaving other specific
target RNA by recognizing RNA molecule.
ACCESSION BD143502
VERSION BD143502.1 GI:27849260
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Taira,K., Warashina,M. and Warashina,T.
TITLE Nucleic acid enzyme acquiring activity of cleaving other specific
target RNA by recognizing RNA molecule
JOURNAL Patent: JP 2002119283-A 5 23-APR-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
SCIENCE AND P T BAKRIE AND BROTHERS,JAPAN BIO INDUSTRY ASSOCIATION,
TECHNOLOGY
COMMENT
OS Artificial Sequence
PN JP 2002119283-A/5
PD 23-APR-2002
PF 13-OCT-2000 JP 2000313320
PI KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO WARASHINA PC
C12N15/09,A61K9/127,A61K38/46,A61K48/00,A61P31/12,A61P35/00, PC
C12N1/15,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/25,C12Q1/68,C12N15/
00,A61K37/54,
PC C12N5/00
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FH Key Location/Qualifiers
ET Source 1..88
FT /organism="Artificial Sequence".
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Db      61  TTCGAAACCGGGCACTACAAACCA 85

RESULT 10
LOCUS   AB080621                153 bp    DNA    linear    SYN 21-MAY-2003
DEFINITION   Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
ACCESSION   AB080621
VERSION     AB080621.1 GI:22531654
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
            Nishino,K., Nakayama,A. and Taira,K.
TITLE       Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL     Unpublished
AUTHORS     Tachi,C.
JOURNAL     Direct Submission
SUBMITTED   (27-FEB-2002) Chikashi Tachi, Azabu University School of
VETERINARY Medicine, Lab. Developmental and Reproductive
BIOTECHNOLOGY; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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/feature="derived from ribozyme"
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Best Local Similarity 75.3%; Pred. NO. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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Best Local Similarity 75.3%; Pred. NO. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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RESULT 11
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ACCESSION   AB080622
VERSION     AB080622.1 GI:22531655
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SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
            Nishino,K., Nakayama,A. and Taira,K.
TITLE       Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL     Unpublished
AUTHORS     Tachi,C.
JOURNAL     Direct Submission
SUBMITTED   (27-FEB-2002) Chikashi Tachi, Azabu University School of
VETERINARY Medicine, Lab. Developmental and Reproductive
BIOTECHNOLOGY; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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Query Match 58.0%; Score 81.8; DB 12; Length 153;
Best Local Similarity 75.3%; Pred. NO. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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QY      61  UUCGAAACCGGGACUACAAACCA 85
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Db      61  TTCGAAACCGGGCACTACAAACCA 85

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TITLE      Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 153)
AUTHORS     Tachi,C.
TITLE      Direct Submission
SUBMITTED   (27-FEB-2002) Chikashi Tachi, Azabu University School of
VETERINARY Medicine, Lab. Developmental and Reproductive
BIOTECHNOLOGY; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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Query Match 58.0%; Score 81.8; DB 12; Length 153;
Best Local Similarity 75.3%; Pred. NO. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION   Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
ACCESSION   AB080623
VERSION     AB080623.1 GI:22531656
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
            Nishino,K., Nakayama,A. and Taira,K.
TITLE      Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL     Unpublished
AUTHORS     Tachi,C.
JOURNAL     Direct Submission
SUBMITTED   (27-FEB-2002) Chikashi Tachi, Azabu University School of
VETERINARY Medicine, Lab. Developmental and Reproductive
BIOTECHNOLOGY; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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1 (bases 1 to 141)
Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
Slidable functional chimeric molecule
Patent: JP 2001190282-A 52 17-JUL-2001;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
SCIENCE AND MANABU NAKAJIMA TECHNOLOGY, KAZUNARI TAIRA
OS Artificial Sequence
PN JP 2001190282-A/52
PD 17-JUL-2001
PF 02-NOV-2000 JP 2000336082
PI KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI PI
KANASAKI
PC
C12N15/09,A61K31/7105,A61K31/1711,A61K38/00,A61P31/12, PC
A61P43/00,
PC C12N9/22,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00, PC
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Matches 77; Conservative 20; Mismatches 24; Indels 0; Gaps 0;
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Db 1 ACCGTGGTTTCGGTAGTGATGTTATCGTTCGCTAACACGCGGAAAGGTCGCCGG 60
QY 61 UUCGAAACCGGCGACUACACCAACACACACACGUGAGGAGCGGAAAGGUCGGAAC 120
Db 1 TCGAAACCGGCGACTACAAACCAACCACTTCTAGATTGTGAACCTGATGAGCGCGAAAG 120
QY 121 G 121
Db 121 G 121
RESULT 8
AB080619 Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
LOCUS tRNAantiSryR24.
DEFINITION
ACCESSION AB080619.1 GI:22531652
VERSION AB080619.1
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
Nishino,K., Nakayama,A. and Taira,K.
TITLE Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 153)
AUTHORS Tachi,C.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
Veterinary Medicine, Lab. Developmental and Reproductive
Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_RNA 1..153
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misc_feature 1..87
/derived from tRNA
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/derived from ribozyme
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Best Local Similarity 75.3%; Pred. No. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;
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Db 1 ACCGTGGTTTCGGTAGTGATGTTATCGTTCGCTAACACGCGGAAAGGTCGCCGG 60
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Db 61 TCGAAACCGGCGACTACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 85
RESULT 9
AB080620 Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
LOCUS tRNAantiSryR23.
DEFINITION
ACCESSION AB080620
VERSION AB080620.1 GI:22531653
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
Nishino,K., Nakayama,A. and Taira,K.
TITLE Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 153)
AUTHORS Tachi,C.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
Veterinary Medicine, Lab. Developmental and Reproductive
Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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trnaantiSryR23
/function="anti murine Sry ribozyme"
misc_feature 1..87
/derived from tRNA
misc_feature 88..153
/derived from ribozyme
BASE COUNT 35 a 41 c 35 g 42 t
ORIGIN
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Best Local Similarity 75.3%; Pred. No. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;
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Best Local Similarity		70.8%;	Pred. No. 1.9e-13;	
Matches	68;	Conservative	20;	Mismatches 8; Indels 0; Gaps 0;
QY	1	ACCGUUGUUCCGUGAGUGUAGUGUUUACACGUGGCCUUAACACGCCGAAAGGUCGCCGG	60	
DB	1	ACCGTGTGTTCCGTTAGTGTATAGTGGTTATACGCTTCGCTTAACACGCCGAAAGGTCGCCGG	60	
QY	61	UUCGAAACCGGGCAGUACAAACCAACACACACACACU 96		
DB	61	TTCGAAACCGGGCAGTACAAACCAACCAACCAAAAT 96		
RESULT 6				
AXI38491			141 bp	mRNA
LOCUS			Sequence 52 from Patent EP1097993.	linear
DEFINITION			AXI38491	PAT 30-MAY-2001
ACCESSION			AXI38491.1	
VERSION			GI:14274387	
KEYWORDS				
SOURCE			synthetic construct	
ORGANISM			synthetic construct	
REFERENCE			artificial sequences.	
1				
AUTHORS			Taira, K., Warashina, M., Kuwabara, T. and Kawasaki, H.	
TITLE			Functional ribozyme chimeric molecules capable of sliding	
JOURNAL			Patent: EP 1097993-A 52 09-MAY-2001;	
			Secretary of Agency of Industrial Science and Technology (JP) ;	
			Taira, Kazunari (JP)	
FEATURES			Location/Qualifiers	
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			/mol_type="mRNA"	
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BASE COUNT	37 a	37 c	35 g	32 t
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QY	1	ACCGUUGUUCCGUGAGUGUAGUGUUUACACGUGGCCUUAACACGCCGAAAGGUCGCCGG	60	
DB	1	ACCGTGTGTTCCGTTAGTGTATAGTGGTTATACGCTTCGCTTAACACGCCGAAAGGTCGCCGG	60	
QY	61	UUCGAAACCGGGCAGUACAAACCAACACACACACUAGGAGGACGAAAGGUCGGAAC	120	
DB	61	TTCGAAACCGGGCAGTACAAACCAACCAACTTCTAGATTGTACCTGTATGAGCGCCGAAG	120	
QY	121 g	121		
DB	121 g	121		
RESULT 7				
BD015659			141 bp	RNA
LOCUS			Slidable functional chimeric molecule.	linear
DEFINITION			BD015659	PAT 27-AUG-2002
ACCESSION			BD015659	
VERSION			BD015659.1	
KEYWORDS			GI:22556796	
SOURCE			JP 2001190282-A/52.	
ORGANISM			synthetic construct	

Db	1	ACCGTTGGTTCCCGTAGTGTAGTGGTTATCACGTTGCCTTAACACGCGAAAGTCCCGG	60
QY	61	UUCGAAACCGGGCACUACAAACCAACCAACAACAACACUAGUAGGAGGACCGAAAGGUCGGAAC	120
Db	61	TTCGAAACCGGGCACTACAA-----ACACACACTGATGAGGACCGCAAGGTCGGAAC	114
QY	121	GGGCACGUCGGAACGGUUUU 141	
Db	115	GGGCACGTCGGAACGGGTTT 135	
RESULT 3			
LOCUS	BD174680		
DEFINITION	Ribozyme expression system.	175 bp	DNA
ACCESSION	BD174680		linear
VERSION	BD174680.1 GI:29120370		PAT 18-MAR-2003
KEYWORDS	JP 2002262880-A/6.		
SOURCE	synthetic construct		
ORGANISM	artificial constructs.		
REFERENCE	1 (bases 1 to 175)		
AUTHORS	Takebe,Y. and Okawa,J.		
TITLE	Ribozyme expression system		
JOURNAL	Patent: JP 2002262880-A 6 17-SEP-2002;		
COMMENT	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, YUTAKA TAKEBE,JUN OKAWA		
	OS Artificial Sequence		
	PN JP 2002262880-A/6		
	PD 17-SEP-2002		
	PF 09-MAR-2001 JP 2001067253		
	PI YUTAKA TAKEBE,JUN OKAWA		
	PC C12N15/09,A61K31/711,A61K35/76,A61K48/00,A61P31/18,C12N5/10,		
	PC C12N9/00,		
	PC C12N15/00,C12N5/00		
	CC Description of Artificial Sequence: the		
	nucleotide sequence of		
	CC ribozyme		
	CC expressing cassette of the invention		
	PH Key Location/Qualifiers		
	FT source 1..175		
FEATURES	Location/Qualifiers		
Source	1..175		
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	/mol_type='genomic DNA'		
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BASE COUNT	48 a 40 c 41 g 46 t		
ORIGIN			
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	Best Local Similarity 69.9%; Pred.No. 6.le-17;		
	Matches 102; Conservative 26; Mismatches 13; Indels 5; Gaps 2		
QY	1	ACCGTUGGUUUCGGUAGUGUAGUACGUGCCUACACGCGAAAGGUCGCCG 60	
Db	29	ACCGTTGGTTCCCGTAGTGTAGTGGTTATCACGTTGCCTTAACACGCGAAAGTCCCGG 88	
QY	61	UUCGAAACCGGGCACUACAAA-----CCAACAACAACAACUAGUAGGACCGCAAGGUCG 116	
Db	89	TTCAAGACCGGGCACTACAAAACCAACGCGATAGTGTGATGAGGACCGCAAGGTCG 148	
QY	117	AAAC-GGGCAGCUGGAAACGGUUUU 141	
Db	149	AAACTTGACACTCCGGAACGGTTT 174	
RESULT 4			
LOCUS	BD174679		
DEFINITION	Ribozyme expression system.	175 bp	DNA
ACCESSION	BD174679		linear
	PAT 18-MAR-2003		

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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 09:38:16 : Search time 1435.54 Seconds
(without alignments)
4018.170 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accgucguuuccgagugu.....ggcacgucggaacgguuu 141

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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40: em.htgo_mus.*

41: em.htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	141	100.0	142	6	E33204	E33204 Expression
2	119	84.4	136	6	E33203	E33203 Expression
3	95.2	67.5	175	6	BD174680	BD174680 Ribozyme
4	91.8	65.1	175	6	BD174679	BD174679 Ribozyme
5	83.2	59.0	100	6	E47174	E47174 Method for
6	82.6	58.6	141	6	AX138491	AX138491 Sequence
7	82.6	58.6	141	6	BD015659	BD015659 Slidable
8	81.8	58.0	153	12	AB080619	AB080619 Synthetic
9	81.8	58.0	153	12	AB080620	AB080620 Synthetic
10	81.8	58.0	153	12	AB080621	AB080621 Synthetic
11	81.8	58.0	153	12	AB080622	AB080622 Synthetic
12	81.8	58.0	153	12	AB080623	AB080623 Synthetic
13	81.8	58.0	153	12	AB080624	AB080624 Synthetic
14	81	57.4	88	6	AX453846	AX453846 Sequence
15	81	57.4	88	6	BD143502	BD143502 Nucleic a
16	81	57.4	88	6	BD182356	BD182356 Novel max
17	81	57.4	117	6	BD174675	BD174675 Ribozyme
18	81	57.4	137	6	AX429079	AX429079 Sequence
19	81	57.4	137	6	BD143601	BD143601 Method of
20	81	57.4	138	6	AX453858	AX453858 Sequence
21	81	57.4	142	6	AX138488	AX138488 Sequence
22	81	57.4	142	6	AX138489	AX138489 Sequence
23	81	57.4	142	6	AX138490	AX138490 Sequence
24	81	57.4	142	6	AX138492	AX138492 Sequence
25	81	57.4	142	6	BD015656	BD015656 Slidable
26	81	57.4	142	6	BD015657	BD015657 Slidable
27	81	57.4	142	6	BD015658	BD015658 Slidable
28	81	57.4	142	6	BD015660	BD015660 Slidable
29	81	57.4	151	6	AX138449	AX138449 Sequence
30	81	57.4	151	6	BD015617	BD015617 Slidable
31	81	57.4	320	6	AX138450	AX138450 Sequence
32	81	57.4	320	6	BD015618	BD015618 Slidable
33	75	53.2	128	6	E33205	E33205 Expression
34	73.4	52.1	149	6	E33207	E33207 Expression
35	73	51.8	95	6	AX138447	AX138447 Sequence
36	73	51.8	95	6	BD015615	BD015615 Slidable
37	73	51.8	95	6	E33206	E33206 Expression
38	73	51.8	183	11	G31283	G31283 sy905g1-L H
39	73	51.8	1396	9	HUMETV1A	M15782 Human HtV1
40	73	51.8	139904	9	HS97D16	AL009179 Human DNA
41	69.8	49.5	132	6	AR041184	AR041184 Sequence
42	69.8	49.5	132	6	AR113038	AR113038 Sequence
43	69.8	49.5	132	6	I66463	I66463 Sequence 17
44	69.8	49.5	265074	2	AC103024	AC103024 Rattus no
45	69.8	49.5	315861	2	AC109931	AC109931 Rattus no

ALIGNMENTS

RESULT 1
E33204
LOCUS
DEFINITION
Accession
E33204
VERSION
E33204.1 GI:18623998
KEYWORDS
JP 2000069972-A/2.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 142)
Tabira,K., Okawa,A. and Ozeki,S.
Expression system for functional nucleic acid transcription
Patent: JP 2000069972-A 2 07-MAR-2000;
JOURNAL
AGENCY OF IND SCIENCE & TECHNOL

E33204
Expression system for functional nucleic acid transcription.
142 bp RNA linear PAT 31-JAN-2002
G31283 sy905g1-L H
M15782 Human HtV1
AL009179 Human DNA
AR041184 Sequence
AR113038 Sequence
I66463 Sequence 17
AC103024 Rattus no
AC109931 Rattus no

Db 91 GGTTTCTATGGTGTAGTMTTACACACGCTGGCCCTACACATGGAAGGTCTCTATTGAA 150

QY 67 AC 68

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Db 151 AC 152

Search completed: September 13, 2003, 09:43:48
Job time : 164.75 secs


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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13960
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13960

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Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGUUGUUCGAGUGUAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUU 62
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Db 241 CGAAACCGGC 231
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RESULT 6
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; Sequence 13961, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13961
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13961

Query Match
Best Local Similarity 46.7%; Score 65.8; DB 13; Length 704;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

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QY 3 CGUUGUUCGAGUGUAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUU 62
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 301 YGCAGGTTCCGTAGTGTAGTGTATCATCGTTCGCTCACACGCGAAAGGTCGCCGTT 242
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 63 CGAAACCGGC 73
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Db 241 CGAAACCGGC 231
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RESULT 7
US-10-027-632-150959

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; Sequence 150959, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150959
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-150959

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Query Match
Best Local Similarity 43.4%; Score 61.2; DB 13; Length 818;
Matches 46; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

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    : ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 239 TGGTTCCGTAGTGTAGTGTATCATCGTTCGCTCACACGCGAAAGGTCGCCGTT 298
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 66 AACCGG 71
    |||
Db 299 AACTGG 304
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```

RESULT 8
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; Sequence 150960, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150960
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Human

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US-09-974-974-17
; Sequence 17, Application US/09974974
; Publication NO. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 138
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVAL T-MzL
US-09-974-974-17

Query Match 57.4%; Score 81; DB 11; Length 138;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUUGUUUCCGUGAGUGAGUUAUACAGUUGCCUACACGCGAAAGGUCCCCGG 60
Db 1 ACCGUUGUUUCCGUGAGUGAGUUAUACAGUUGCCUACACGCGAAAGGUCCCCGG 60

QY 61 UUGCAACCGGGCACUACAAA 81
Db 61 UUGCAACCGGGCACUACAAA 81

RESULT 3
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; Sequence 13958, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13958
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13958

Query Match 46.7%; Score 65.8; DB 13; Length 704;
Best Local Similarity 71.8%; Pred. No. 1.2e-13;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

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 Db YCAGGTTTCGGTGTAGTGTAGTGGTTATACAGTTGGCGCTACACGCGAAAGGTCGCCGGTT 242
 QY 63 CGAAACCGGGC 73
 Db 241 CGAAACCGGGC 231

RESULT 4
 US-10-027-632-13959/c
 ; Sequence 13959, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827.129
 ; CURRENT APPLICATION NUMBER: US/10/027.632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
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 ; ORGANISM: Human
 US-10-027-632-13959

Query Match 46.7%; Score 65.8; DB 13; Length 704;
 Best Local Similarity 71.8%; Pred. No. 1.2e-13;
 Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0

QY 3 CGUUGGUUUCCGAGUGAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCGCCGGUU 62
 Db YCAGGTTTCGGTGTAGTGTAGTGGTTATACAGTTGGCGCTACACGCGAAAGGTCGCCGGTT 242
 QY 63 CGAAACCGGGC 73
 Db 241 CGAAACCGGGC 231

RESULT 5
 US-10-027-632-13960/c
 ; Sequence 13960, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827.129
 ; CURRENT APPLICATION NUMBER: US/10/027.632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363

QY 3 CGUUGGUUUCCGAGUGAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCGCCGGUU 62
 Db YCAGGTTTCGGTGTAGTGTAGTGGTTATACAGTTGGCGCTACACGCGAAAGGTCGCCGGTT 242
 QY 63 CGAAACCGGGC 73
 Db 241 CGAAACCGGGC 231

RESULT 4
 US-10-027-632-13959/c
 ; Sequence 13959, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827.129
 ; CURRENT APPLICATION NUMBER: US/10/027.632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13959
 ; LENGTH: 704
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-13959

Query Match 46.7%; Score 65.8; DB 13; Length 704;
 Best Local Similarity 71.8%; Pred. No. 1.2e-13;
 Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0

QY 3 CGUUGGUUUCCGAGUGAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCGCCGGUU 62
 Db YCAGGTTTCGGTGTAGTGTAGTGGTTATACAGTTGGCGCTACACGCGAAAGGTCGCCGGTT 242
 QY 63 CGAAACCGGGC 73
 Db 241 CGAAACCGGGC 231

RESULT 5
 US-10-027-632-13960/c
 ; Sequence 13960, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827.129
 ; CURRENT APPLICATION NUMBER: US/10/027.632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 08:02:46 ; Search time 152.75 Seconds
(without alignments)
2241.006 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	81	57.4	88	11	US-09-974-974-5
2	81	57.4	138	11	US-09-974-974-17
3	65.8	46.7	704	13	US-10-027-632-13958
4	65.8	46.7	704	13	US-10-027-632-13959
5	65.8	46.7	704	13	US-10-027-632-13960
6	65.8	46.7	704	13	US-10-027-632-13961
7	61.2	43.4	818	13	US-10-027-632-150959
8	61.2	43.4	818	13	US-10-027-632-150960
9	50.6	35.9	603	13	US-10-027-632-135532
10	50	35.5	817	13	US-10-027-632-135520
11	48.4	34.3	871	13	US-10-027-632-148440
12	41.6	29.5	118067	15	US-10-081-327-32
13	40	28.4	11103	12	US-10-056-405-23
14	40	28.4	11103	14	US-10-094-240-23
15	39.6	28.1	322	13	US-10-027-632-272410
16	38.6	27.4	2126	12	US-10-325-107-59

17	37.4	26.5	999	9	US-09-842-552-100	Sequence 100, App
18	37.4	26.5	2336	9	US-09-842-552-102	Sequence 102, App
19	37.4	26.5	5048	11	US-09-884-465A-2	Sequence 2, Appli
20	36.2	25.7	9425	8	US-08-781-986A-87	Sequence 87, Appl
21	36	25.5	440	9	US-09-864-761-10165	Sequence 10165, A
22	36	25.5	740	10	US-09-070-927A-846	Sequence 846, App
23	35.4	25.1	400	8	US-08-781-986A-3707	Sequence 3707, Ap
24	34.8	24.7	400	8	US-08-781-986A-3777	Sequence 3777, Ap
25	34.6	24.5	400	8	US-08-781-986A-3809	Sequence 3809, Ap
26	34.6	24.5	6591	8	US-08-781-986A-3114	Sequence 3114, Ap
27	34.2	24.3	214	9	US-09-815-242-3628	Sequence 3628, Ap
28	34.2	24.3	400	8	US-08-781-986A-3650	Sequence 3650, Ap
29	34.2	24.3	400	8	US-08-781-986A-3736	Sequence 3736, Ap
30	34.2	24.3	449	8	US-08-781-986A-3687	Sequence 3687, Ap
31	34.2	24.3	619	8	US-08-781-986A-3571	Sequence 3571, Ap
32	34	24.1	687	8	US-08-781-986A-608	Sequence 608, App
33	33	23.4	3309400	10	US-09-738-626-1	Sequence 1, Appli
34	31.2	22.1	508	10	US-09-917-800A-319	Sequence 319, App
35	30	21.3	4792	10	US-09-863-040-5	Sequence 5, Appli
36	29.6	21.0	1218	10	US-09-974-300-308	Sequence 308, App
37	29.4	20.9	780	10	US-09-738-626-750	Sequence 750, App
38	29.2	20.7	9025608	14	US-10-156-761-1	Sequence 1, Appli
39	29	20.6	6526	12	US-10-311-455-2210	Sequence 2210, Ap
40	28.8	20.4	5109	11	US-09-962-298-2	Sequence 2, Appli
41	28.6	20.3	124884	11	US-09-913-514-1	Sequence 1, Appli
42	28.6	20.3	124884	12	US-10-288-823-76	Sequence 76, Appli
43	28.6	20.3	125157	11	US-09-913-514-2	Sequence 2, Appli
44	28.4	20.1	611	13	US-10-027-632-199163	Sequence 199163,
45	28.4	20.1	611	13	US-10-027-632-199164	Sequence 199164,

ALIGNMENTS

RESULT 1

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; Sequence 5, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; FILE REFERENCE: target RNA by recognizing another molecule
; CURRENT APPLICATION NUMBER: US/09/974,974
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAval promoter sequence
US-09-974-974-5
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Query Match 57.4%; Score 81; DB 11; Length 88;
Best Local Similarity 100.0%; Pred. NO. 2.7e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCUGUGUUCGGUGUGUGUGUUCACGUCGUCGACGCGAAGGCCCGG 60
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QY 61 UUCGAAACCGGCGACUACAAA 81
    |||||
Db 61 UUCGAAACCGGCGACUACAAA 81
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RESULT 2